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(54) Title: COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER			
(57) Abstract			
<p>Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate tumor protein, or mRNA encoding such a protein, in a sample are also provided.</p>			

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COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER

TECHNICAL FIELD

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides comprising at least a portion of a prostate tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for prevention and treatment of prostate cancer, and for the diagnosis and monitoring of such cancers.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for the diagnosis and therapy of cancer, such as prostate cancer. In one aspect, the present

invention provides polypeptides comprising at least a portion of a prostate tumor protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; (b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and (c) complements of any of the sequence of (a) or (b). In certain specific embodiments, such a polypeptide comprises at least a portion, or variant thereof, of a tumor protein that includes an amino acid sequence selected from the group consisting of sequences recited in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a prostate tumor protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and a non-specific immune response enhancer.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a prostate tumor protein; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a non-specific immune response enhancer.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

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Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a non-specific immune response enhancer.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a prostate tumor protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited

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above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be prostate cancer.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic

kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate tumor polypeptide P502S, as compared to control fibroblasts. The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate tumor polypeptide P502S. In each case, the number of γ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/*neu*.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate tumor polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a CD8⁺ cell line (3A-1) for a representative prostate tumor antigen (P501S). Figure 6A shows the results of a ⁵¹Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

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SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12
 SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16
 SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1
 SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9
 SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4
 SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17
 SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17
 SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12
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 SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862
 SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862
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 SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19
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 SEQ ID NO: 22 is the determined 5' cDNA sequence for K1-58
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 SEQ ID NO: 26 is the determined 5' cDNA sequence for L1-4
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 SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16
 SEQ ID NO: 32 is the determined 3' cDNA sequence for J1-21
 SEQ ID NO: 33 is the determined 3' cDNA sequence for K1-48
 SEQ ID NO: 34 is the determined 3' cDNA sequence for K1-55
 SEQ ID NO: 35 is the determined 3' cDNA sequence for L1-2
 SEQ ID NO: 36 is the determined 3' cDNA sequence for L1-6
 SEQ ID NO: 37 is the determined 3' cDNA sequence for N1-1858
 SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860
 SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861

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SEQ ID NO: 40 is the determined 3' cDNA sequence for N1-1864
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 SEQ ID NO: 73 is the determined cDNA sequence for V1-3686
 SEQ ID NO: 74 is the determined cDNA sequence for R1-2330
 SEQ ID NO: 75 is the determined cDNA sequence for 1B-3976
 SEQ ID NO: 76 is the determined cDNA sequence for V1-3679

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SEQ ID NO: 77 is the determined cDNA sequence for 1G-4736
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 SEQ ID NO: 85 is the determined cDNA sequence for 1H-4787
 SEQ ID NO: 86 is the determined cDNA sequence for 1H-4796
 SEQ ID NO: 87 is the determined cDNA sequence for 1I-4807
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 SEQ ID NO: 108 is the predicted amino acid sequence for F1-12
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 SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12
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 SEQ ID NO: 112 is the predicted amino acid sequence for J1-17

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SEQ ID NO: 126 is the determined cDNA sequence for P124
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SEQ ID NO: 129 is the determined cDNA sequence for P133
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 SEQ ID NO: 200 is the determined extended cDNA sequence for 1D-4309
 SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-4278
 SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-4288
 SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-4283
 SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-4304
 SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-4296
 SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-4280
 SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd
 SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con
 SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev
 SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd
 SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev
 SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd
 SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev
 SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd
 SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev
 SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd
 SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev
 SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd
 SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev
 SEQ ID NO: 220 is the determined cDNA sequence for 8-h1 lrev
 SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd
 SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev
 SEQ ID NO: 223 is the determined cDNA sequence for P509S

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SEQ ID NO: 224 is the determined cDNA sequence for P510S
 SEQ ID NO: 225 is the determined cDNA sequence for P703DE5
 SEQ ID NO: 226 is the determined cDNA sequence for 9-A11
 SEQ ID NO: 227 is the determined cDNA sequence for 8-C6
 SEQ ID NO: 228 is the determined cDNA sequence for 8-H7
 SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13
 SEQ ID NO: 230 is the determined cDNA sequence for JPTPN14
 SEQ ID NO: 231 is the determined cDNA sequence for JPTPN23
 SEQ ID NO: 232 is the determined cDNA sequence for JPTPN24
 SEQ ID NO: 233 is the determined cDNA sequence for JPTPN25
 SEQ ID NO: 234 is the determined cDNA sequence for JPTPN30
 SEQ ID NO: 235 is the determined cDNA sequence for JPTPN34
 SEQ ID NO: 236 is the determined cDNA sequence for PTPN35
 SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36
 SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38
 SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39
 SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40
 SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41
 SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42
 SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45
 SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46
 SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51
 SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56
 SEQ ID NO: 247 is the determined cDNA sequence for PTPN64
 SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65
 SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67
 SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76
 SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84
 SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85
 SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86
 SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87
 SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88
 SEQ ID NO: 256 is the determined cDNA sequence for JP1F1
 SEQ ID NO: 257 is the determined cDNA sequence for JP1F2
 SEQ ID NO: 258 is the determined cDNA sequence for JP1C2
 SEQ ID NO: 259 is the determined cDNA sequence for JP1B1
 SEQ ID NO: 260 is the determined cDNA sequence for JP1B2

SEQ ID NO: 261 is the determined cDNA sequence for JP1D3
SEQ ID NO: 262 is the determined cDNA sequence for JP1A4
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6
SEQ ID NO: 266 is the determined cDNA sequence for JP1B5
SEQ ID NO: 267 is the determined cDNA sequence for JP1A6
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9
SEQ ID NO: 271 is the determined cDNA sequence for JP1C10
SEQ ID NO: 272 is the determined cDNA sequence for JP1A9
SEQ ID NO: 273 is the determined cDNA sequence for JP1F12
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11
SEQ ID NO: 276 is the determined cDNA sequence for JP1C11
SEQ ID NO: 277 is the determined cDNA sequence for JP1C12
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2
SEQ ID NO: 281 is the determined cDNA sequence for JP8H1
SEQ ID NO: 282 is the determined cDNA sequence for JP8H2
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3
SEQ ID NO: 286 is the determined cDNA sequence for JP8G4
SEQ ID NO: 287 is the determined cDNA sequence for JP8B6
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6
SEQ ID NO: 289 is the determined cDNA sequence for JP8F5
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8
SEQ ID NO: 291 is the determined cDNA sequence for JP8C7
SEQ ID NO: 292 is the determined cDNA sequence for JP8D7
SEQ ID NO: 293 is the determined cDNA sequence for P8D8
SEQ ID NO: 294 is the determined cDNA sequence for JP8E7
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8
SEQ ID NO: 297 is the determined cDNA sequence for JP8B10

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SEQ ID NO: 298 is the determined cDNA sequence for JP8C10
 SEQ ID NO: 299 is the determined cDNA sequence for JP8E9
 SEQ ID NO: 300 is the determined cDNA sequence for JP8E10
 SEQ ID NO: 301 is the determined cDNA sequence for JP8F9
 SEQ ID NO: 302 is the determined cDNA sequence for JP8H9
 SEQ ID NO: 303 is the determined cDNA sequence for JP8C12
 SEQ ID NO: 304 is the determined cDNA sequence for JP8E11
 SEQ ID NO: 305 is the determined cDNA sequence for JP8E12
 SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12
 SEQ ID NO: 307 is the determined cDNA sequence for P711P
 SEQ ID NO: 308 is the determined cDNA sequence for P712P
 SEQ ID NO: 309 is the determined cDNA sequence for CLONE23
 SEQ ID NO: 310 is the determined cDNA sequence for P774P
 SEQ ID NO: 311 is the determined cDNA sequence for P775P
 SEQ ID NO: 312 is the determined cDNA sequence for P715P
 SEQ ID NO: 313 is the determined cDNA sequence for P710P
 SEQ ID NO: 314 is the determined cDNA sequence for P767P
 SEQ ID NO: 315 is the determined cDNA sequence for P768P
 SEQ ID NO: 316-325 are the determined cDNA sequences of previously isolated genes
 SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5
 SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5
 SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26
 SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26
 SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23
 SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23
 SEQ ID NO: 332 is the determined full length cDNA sequence for P509S
 SEQ ID NO: 333 is the determined extended cDNA sequence for P707P (also referred to as 11-C9)
 SEQ ID NO: 334 is the determined cDNA sequence for P714P
 SEQ ID NO: 335 is the determined cDNA sequence for P705P (also referred to as 9-F3)
 SEQ ID NO: 336 is the predicted amino acid sequence for P705P
 SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10
 SEQ ID NO: 338 is the amino acid sequence of the peptide p5
 SEQ ID NO: 339 is the predicted amino acid sequence of P509S
 SEQ ID NO: 340 is the determined cDNA sequence for P778P
 SEQ ID NO: 341 is the determined cDNA sequence for P786P
 SEQ ID NO: 342 is the determined cDNA sequence for P789P

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SEQ ID NO: 343 is the determined cDNA sequence for a clone showing homology to Homo sapiens MM46 mRNA

SEQ ID NO: 344 is the determined cDNA sequence for a clone showing homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA

SEQ ID NO: 345 is the determined cDNA sequence for a clone showing homology to Homo sapiens mRNA for E-cadherin

SEQ ID NO: 346 is the determined cDNA sequence for a clone showing homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase (SHMT)

SEQ ID NO: 347 is the determined cDNA sequence for a clone showing homology to Homo sapiens natural resistance-associated macrophage protein2 (NRAMP2)

SEQ ID NO: 348 is the determined cDNA sequence for a clone showing homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)

SEQ ID NO: 349 is the determined cDNA sequence for a clone showing homology to Human mRNA for proteasome subunit p40

SEQ ID NO: 350 is the determined cDNA sequence for P777P

SEQ ID NO: 351 is the determined cDNA sequence for P779P

SEQ ID NO: 352 is the determined cDNA sequence for P790P

SEQ ID NO: 353 is the determined cDNA sequence for P784P

SEQ ID NO: 354 is the determined cDNA sequence for P776P

SEQ ID NO: 355 is the determined cDNA sequence for P780P

SEQ ID NO: 356 is the determined cDNA sequence for P544S

SEQ ID NO: 357 is the determined cDNA sequence for P745S

SEQ ID NO: 358 is the determined cDNA sequence for P782P

SEQ ID NO: 359 is the determined cDNA sequence for P783P

SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984

SEQ ID NO: 361 is the determined cDNA sequence for P787P

SEQ ID NO: 362 is the determined cDNA sequence for P788P

SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994

SEQ ID NO: 364 is the determined cDNA sequence for P781P

SEQ ID NO: 365 is the determined cDNA sequence for P785P

SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.

SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.

SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.

SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.

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SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.

SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.

SEQ ID NO: 381 is the determined cDNA sequence for B716P.

SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.

SEQ ID NO: 383 is the predicted amino acid sequence for P711P.

SEQ ID NO: 384 is the cDNA sequence for P1000C.

SEQ ID NO: 385 is the cDNA sequence for CGI-82.

SEQ ID NO:386 is the cDNA sequence for 23320.

SEQ ID NO:387 is the cDNA sequence for CGI-69.

SEQ ID NO:388 is the cDNA sequence for L-idoitol-2-dehydrogenase.

SEQ ID NO:389 is the cDNA sequence for 23379.

SEQ ID NO:390 is the cDNA sequence for 23381.

SEQ ID NO:391 is the cDNA sequence for KIAA0122.

SEQ ID NO:392 is the cDNA sequence for 23399.

SEQ ID NO:393 is the cDNA sequence for a previously identified gene.

SEQ ID NO:394 is the cDNA sequence for HCLBP.

SEQ ID NO:395 is the cDNA sequence for transglutaminase.

SEQ ID NO:396 is the cDNA sequence for a previously identified gene.

SEQ ID NO:397 is the cDNA sequence for PAP.

SEQ ID NO:398 is the cDNA sequence for Ets transcription factor PDEF.

SEQ ID NO:399 is the cDNA sequence for hTGR.

SEQ ID NO:400 is the cDNA sequence for KIAA0295.

SEQ ID NO:401 is the cDNA sequence for 22545.

SEQ ID NO:402 is the cDNA sequence for 22547.

SEQ ID NO:403 is the cDNA sequence for 22548.

SEQ ID NO:404 is the cDNA sequence for 22550.

SEQ ID NO:405 is the cDNA sequence for 22551.

SEQ ID NO:406 is the cDNA sequence for 22552.

SEQ ID NO:407 is the cDNA sequence for 22553.

SEQ ID NO:408 is the cDNA sequence for 22558.

SEQ ID NO:409 is the cDNA sequence for 22562.

SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.

SEQ ID NO:412 is the cDNA sequence for 22568.

SEQ ID NO:413 is the cDNA sequence for 22570.

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SEQ ID NO:414 is the cDNA sequence for 22571.
SEQ ID NO:415 is the cDNA sequence for 22572.
SEQ ID NO:416 is the cDNA sequence for 22573.
SEQ ID NO:417 is the cDNA sequence for 22573.
SEQ ID NO:418 is the cDNA sequence for 22575.
SEQ ID NO:419 is the cDNA sequence for 22580.
SEQ ID NO:420 is the cDNA sequence for 22581.
SEQ ID NO:421 is the cDNA sequence for 22582.
SEQ ID NO:422 is the cDNA sequence for 22583.
SEQ ID NO:423 is the cDNA sequence for 22584.
SEQ ID NO:424 is the cDNA sequence for 22585.
SEQ ID NO:425 is the cDNA sequence for 22586.
SEQ ID NO:426 is the cDNA sequence for 22587.
SEQ ID NO:427 is the cDNA sequence for 22588.
SEQ ID NO:428 is the cDNA sequence for 22589.
SEQ ID NO:429 is the cDNA sequence for 22590.
SEQ ID NO:430 is the cDNA sequence for 22591.
SEQ ID NO:431 is the cDNA sequence for 22592.
SEQ ID NO:432 is the cDNA sequence for 22593.
SEQ ID NO:433 is the cDNA sequence for 22594.
SEQ ID NO:434 is the cDNA sequence for 22595.
SEQ ID NO:435 is the cDNA sequence for 22596.
SEQ ID NO:436 is the cDNA sequence for 22847.
SEQ ID NO:437 is the cDNA sequence for 22848.
SEQ ID NO:438 is the cDNA sequence for 22849.
SEQ ID NO:439 is the cDNA sequence for 22851.
SEQ ID NO:440 is the cDNA sequence for 22852.
SEQ ID NO:441 is the cDNA sequence for 22853.
SEQ ID NO:442 is the cDNA sequence for 22854.
SEQ ID NO:443 is the cDNA sequence for 22855.
SEQ ID NO:444 is the cDNA sequence for 22856.
SEQ ID NO:445 is the cDNA sequence for 22857.
SEQ ID NO:446 is the cDNA sequence for 23601.
SEQ ID NO:447 is the cDNA sequence for 23602.
SEQ ID NO:448 is the cDNA sequence for 23605.
SEQ ID NO:449 is the cDNA sequence for 23606.
SEQ ID NO:450 is the cDNA sequence for 23612.

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SEQ ID NO:451 is the cDNA sequence for 23614.
 SEQ ID NO:452 is the cDNA sequence for 23618.
 SEQ ID NO:453 is the cDNA sequence for 23622.
 SEQ ID NO:454 is the cDNA sequence for folate hydrolase.
 SEQ ID NO:455 is the cDNA sequence for LIM protein.
 SEQ ID NO:456 is the cDNA sequence for a known gene.
 SEQ ID NO:457 is the cDNA sequence for a known gene.
 SEQ ID NO:458 is the cDNA sequence for a previously identified gene.
 SEQ ID NO:459 is the cDNA sequence for 23045.
 SEQ ID NO:460 is the cDNA sequence for 23032.
 SEQ ID NO:461 is the cDNA sequence for 23054.
 SEQ ID NOs:462-467 are cDNA sequences for known genes.
 SEQ ID NOs:468-471 are cDNA sequences for P710P.
 SEQ ID NO:472 is a cDNA sequence for P1001C.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer. The compositions described herein may include prostate tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a prostate tumor protein or a variant thereof. A "prostate tumor protein" is a protein that is expressed in prostate tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal tissue, as determined using a representative assay provided herein. Certain prostate tumor proteins are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with prostate cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery of human prostate tumor proteins. Sequences of polynucleotides encoding certain tumor proteins, or portions thereof, are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Sequences of polypeptides comprising at least a portion of a tumor protein are provided in SEQ ID NOs:112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

PROSTATE TUMOR PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a prostate tumor protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a prostate tumor protein. More preferably, a polynucleotide encodes an immunogenic portion of a prostate tumor protein. Polynucleotides complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a prostate tumor protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native prostate tumor protein or a portion thereof.

Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50,

in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenesis pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native prostate tumor protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to

the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a prostate tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as prostate tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion may be used to isolate a full length gene from a suitable library (*e.g.*, a prostate tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using

standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

Certain nucleic acid sequences of cDNA molecules encoding at least a portion of a prostate tumor protein are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Isolation of these

polynucleotides is described below. Each of these prostate tumor proteins was overexpressed in prostate tumor tissue.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a prostate tumor protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (e.g., by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a prostate tumor polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a tumor protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In Huber and Carr, Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (e.g., promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such

as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (*e.g.*, avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

PROSTATE TUMOR POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a prostate tumor protein or a variant thereof, as described herein. As noted above, a "prostate tumor protein" is a protein that is expressed by prostate tumor cells. Proteins that are prostate tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with prostate cancer. Polypeptides as described herein may be of any length. Additional sequences derived from

the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a prostate tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native prostate tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As noted above, a composition may comprise a variant of a native prostate tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native prostate tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein.

Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are

E. coli, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into

the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see*, for example, Stoute et al. *New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as

amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (see *Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a prostate tumor protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a prostate tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a prostate tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a prostate tumor protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, urine and/or tumor biopsies) from

patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g., Harlow and Lane, Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g., mice, rats, rabbits, sheep or goats*). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e., reactivity with the polypeptide of interest*). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient

time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and

thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a prostate tumor protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the CEPRATE™ system, available from CellPro Inc., Bothell WA (*see also* U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a prostate tumor polypeptide, polynucleotide encoding a prostate tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a prostate tumor polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a prostate tumor polypeptide if the T cells kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (*e.g.*, by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a prostate tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (*e.g.*, TNF or IFN-γ) is indicative of T cell activation (*see* Coligan et al., *Current Protocols in Immunology*, vol. 1, Wiley Interscience

(Greene 1998)). T cells that have been activated in response to a prostate tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Prostate tumor protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a prostate tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a prostate tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a prostate tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of a prostate tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and a non-specific immune response enhancer. A non-specific immune response enhancer may be any substance that enhances an immune response to an exogenous antigen. Examples of non-specific immune response enhancers include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998,

and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) and/or

preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6, IL-10 and TNF- β) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is

quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule or sponge that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*) and based on the lack of differentiation markers of B cells (CD19 and CD20), T cells (CD3), monocytes (CD14) and natural killer cells (CD56), as determined using standard assays. Dendritic cells may, of course, be engineered to express specific cell-

surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor, mannose receptor and DEC-205 marker. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80 and CD86).

APCs may generally be transfected with a polynucleotide encoding a prostate tumor protein (or portion or other variant thereof) such that the prostate tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the prostate tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that

provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as prostate cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein

may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al., *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100 μ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such

a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a prostate tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or more prostate tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding

agent. Suitable polypeptides for use within such assays include full length prostate tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred

embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use prostate tumor polypeptides to

detect antibodies that bind to such polypeptides in a biological sample. The detection of such prostate tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a prostate tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a prostate tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with prostate tumor polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of prostate tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a prostate tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a prostate tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the prostate tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a prostate tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a prostate tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers

comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375 and 381. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple prostate tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

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DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a prostate tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a prostate tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a prostate tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a prostate tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

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EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of

H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction I").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human

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autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted

amino acid sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO: 73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and

prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional, studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that

F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression

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in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatzis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. No significant homologies were found to the sequence of P1000C.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated

and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable.

Increased expression of 8-F11 was seen in prostate tumor and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both micro-array technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues.

Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P were found.

Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

EXAMPLE 5

FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JTPN30 (SEQ ID NO: 234; similarity to rat mRNA for proteasome subunit), JTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of GenBank revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349, 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 10 (SEQ ID NO: 340-349) were found to show some homology to previously identified sequences. No significant homologies were found to the clones of SEQ ID NO: 350-365.

EXAMPLE 6

PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

Mice expressing the transgene for human HLA A2.1 (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were immunized with 100µg of P2S#12 and 120µg of an I-A^b binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at 6×10^6 cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL), 2×10^{-5} M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later, cells (5×10^5 /ml) were restimulated with 2.5×10^6 /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman et al, *Science* 258:815-818, 1992) and 3×10^6 /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were

restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2.1 expressing) transduced with P502S than against control fibroblasts. An example is presented in Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2.1 molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200 $\mu\text{g/ml}$ were added to cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes, CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

Mice expressing the transgene for human HLA A2.1 were immunized as described by Theobald et al. (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5 μg of P1S #10 and 120 μg of an I-A^b binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single cell suspensions prepared using a nylon mesh. Cells were then resuspended at 6×10^6 cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed (2 $\mu\text{g/ml}$ P1S#10 and 10mg/ml β 2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7 $\mu\text{g/ml}$ dextran sulfate and 25 $\mu\text{g/ml}$ LPS for 3 days). Six days later cells ($5 \times 10^5/\text{ml}$) were restimulated with $2.5 \times 10^6/\text{ml}$ peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and $3 \times 10^6/\text{ml}$ A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly

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basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

EXAMPLE 7

ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE TUMOR POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.

Human CD8⁺ T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8⁺ T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a γ -interferon ELISPOT assay (see Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on 10^4 fibroblasts in the presence of 3 μ g/ml human β_2 -microglobulin and 1 μ g/ml P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the fibroblasts were treated with 10 ng/ml γ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a γ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of γ -interferon spots with increasing numbers of T

cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

EXAMPLE 8

PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION WITH A PROSTATE ANTIGEN

The prostate tumor antigen L1-12, as described above, is also referred to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with 100 µg VR10132-P501S either intramuscularly or intradermally. The mice were immunized three times, with a two week interval between immunizations. Two weeks after the last immunization, immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL activity was assessed against P501S transduced targets. Two out of 8 mice developed strong anti-P501S CTL responses. These results demonstrate that P501S contains at least one naturally processed A2-restricted CTL epitope.

EXAMPLE 9

GENERATION OF HUMAN CTL *IN VITRO* USING WHOLE GENE PRIMING AND STIMULATION TECHNIQUES WITH PROSTATE TUMOR ANTIGEN

Using *in vitro* whole-gene priming with P501S-retrovirally transduced autologous fibroblasts (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon-γ ELISPOT analysis as described above. Using a panel of HLA-mismatched fibroblast lines transduced with P501S, these CTL lines were shown to be restricted HLA-A2 class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3 µg/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8+ T cells were isolated using a magnetic bead system, and

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priming cultures were initiated using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S. Following four stimulation cycles, CD8⁺ T cell lines were identified that specifically produced interferon- γ when stimulated with P501S-transduced autologous fibroblasts. The P501S-specific activity could be sustained by the continued stimulation of the cultures with P501S-transduced fibroblasts in the presence of IL-15. A panel of HLA-mismatched fibroblast lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon- γ in an ELISPOT assay, the P501S specific response was shown to be restricted by HLA-A2. These results demonstrate that a CD8⁺ CTL response to P501S can be elicited.

EXAMPLE 10

IDENTIFICATION OF A NATURALLY PROCESSED CTL EPIOTOPE CONTAINED WITHIN A PROSTATE TUMOR ANTIGEN

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific CD8⁺ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2 transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of P703P transduced target cells expressing either HLA-A2Kb or HLA-A2. Specifically, HLA-A2 transgenic mice were immunized subcutaneously in the footpad with 100 μ g of p5 peptide together with 140 μ g of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with p5 peptide and cultured with GM-CSF and IL-4 together with CD8⁺ T cell enriched PBMC. CTL lines were restimulated on a weekly basis

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with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures, CTL recognition of p5-pulsed target cells was demonstrated.

EXAMPLE 11

EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN IN PROSTATE

Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences for these splice forms are provided in SEQ ID NO: 366-375, with the predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that B305D is highly expressed in breast tumor, prostate tumor, normal prostate tumor and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach).

EXAMPLE 12

ELICITATION OF PROSTATE TUMOR ANTIGEN-SPECIFIC CTL RESPONSES IN HUMAN BLOOD

This Example illustrates the ability of a prostate tumor antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GMCSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8⁺ cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles, CD8⁺ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to

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express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays (^{51}Cr release) and interferon-gamma production (Interferon-gamma Elispot; *see above* and Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). The results of these assays are presented in Figures 6A and 6B.

EXAMPLE 13

IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-400) correspond to known sequences, as shown in Table I.

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Table I

Summary of Prostate Tumor Antigens

Known Genes	Previously identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang(23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	

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transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-iditol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate

tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2 bangur showed 23.25 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97% of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

EXAMPLE 14

IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate tumor antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups, Plus (normal prostate and prostate tumor libraries, and breast cell lines, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

Table II
Prostate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups: Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones found in the Plus and Other group libraries only; no expression detected in the Minus group; Type 3- EST clones found in the Plus, Minus and Other group libraries, but the expression in the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones found in Plus, Minus and Other group libraries, but the expression in the Plus group is higher than the expression in the Minus group. This analysis identified 4,345 breast clusters (*see* Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

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Table III
Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

The inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor cDNA was at least three times the level in normal prostate cDNA) were identified as prostate tumor-specific sequences (Table IV). The sequences of these clones are provided in SEQ ID NOs:401-453, with certain novel sequences shown in SEQ ID NOs:407, 413, 416-419, 422, 426, 427 and 450.

Table IV
Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P

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403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57

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439	22851	PAP
440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

EXAMPLE 15

FURTHER IDENTIFICATION OF PROSTATE TUMOR ANTIGENS
BY MICROARRAY ANALYSIS

This Example describes the isolation of additional prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NOs:454-467. Of these sequences SEQ ID NOs:459-461 correspond to novel genes. The others (SEQ ID NOs:454-458 and 461-467) correspond to known sequences.

EXAMPLE 16

FURTHER CHARACTERIZATION OF PROSTATE TUMOR ANTIGEN P710P

This Example describes the full length cloning of P710P.

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The prostate cDNA library described above was screened with the P710P fragment described above. One million colonies were plated on LB/Ampicillin plates. Nylon membrane filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic ABI Sequencer. Four sequences were obtained, and are presented in SEQ ID NOs:468-471.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the present invention is not limited except as by the appended claims.

CLAIMS

1. An isolated polypeptide comprising at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472;

(b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and

(c) complements of any of the sequence of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotide sequences.

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 108, 112, 113, 114, 172, 176, 178, 327, 329, 331, 339 and 383.

4. An isolated polynucleotide encoding at least 15 amino acid residues of a prostate tumor protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434,

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435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

6. An isolated polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

7. An isolated polynucleotide comprising a sequence that hybridizes, under moderately stringent conditions, to a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector comprising a polynucleotide according to any one of claims 4-7.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An expression vector comprising a polynucleotide according claim 8.

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12. A host cell transformed or transfected with an expression vector according to claim 11.

13. A pharmaceutical composition comprising a polypeptide according to claim 1, in combination with a physiologically acceptable carrier.

14. A vaccine comprising a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.

15. A vaccine according to claim 14, wherein the non-specific immune response enhancer is an adjuvant.

16. A vaccine according to claim 14, wherein the non-specific immune response enhancer induces a predominantly Type I response.

17. A pharmaceutical composition comprising a polynucleotide according to claim 4, in combination with a physiologically acceptable carrier.

18. A vaccine comprising a polynucleotide according to claim 4, in combination with a non-specific immune response enhancer.

19. A vaccine according to claim 18, wherein the non-specific immune response enhancer is an adjuvant.

20. A vaccine according to claim 18, wherein the non-specific immune response enhancer induces a predominantly Type I response.

21. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a prostate tumor protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472 or a complement of any of the foregoing polynucleotide sequences.

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22. A pharmaceutical composition comprising an antibody or fragment thereof according to claim 18, in combination with a physiologically acceptable carrier.

23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.

25. A vaccine comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.

26. A vaccine according to claim 25, wherein the non-specific immune response enhancer is an adjuvant.

27. A vaccine according to claim 25, wherein the non-specific immune response enhancer induces a predominantly Type I response.

28. A vaccine according to claim 25, wherein the antigen-presenting cell is a dendritic cell.

29. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

30. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polynucleotide according to claim 4, and thereby inhibiting the development of a cancer in the patient.

31. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antibody or antigen-binding fragment thereof according to claim 21, and thereby inhibiting the development of a cancer in the patient.

32. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

33. A method according to claim 32, wherein the antigen-presenting cell is a dendritic cell.

34. A method according to any one of claims 29-32, wherein the cancer is prostate cancer.

35. A fusion protein comprising at least one polypeptide according to claim 1.

36. A fusion protein according to claim 35, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

37. A fusion protein according to claim 35, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

38. A fusion protein according to claim 35, wherein the fusion protein comprises an affinity tag.

39. An isolated polynucleotide encoding a fusion protein according to claim 35.

40. A pharmaceutical composition comprising a fusion protein according to claim 32, in combination with a physiologically acceptable carrier.

41. A vaccine comprising a fusion protein according to claim 35, in combination with a non-specific immune response enhancer.

42. A vaccine according to claim 41, wherein the non-specific immune response enhancer is an adjuvant.

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43. A vaccine according to claim 41, wherein the non-specific immune response enhancer induces a predominantly Type I response.

44. A pharmaceutical composition comprising a polynucleotide according to claim 40, in combination with a physiologically acceptable carrier.

45. A vaccine comprising a polynucleotide according to claim 40, in combination with a non-specific immune response enhancer.

46. A vaccine according to claim 45, wherein the non-specific immune response enhancer is an adjuvant.

47. A vaccine according to claim 45, wherein the non-specific immune response enhancer induces a predominantly Type I response.

48. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 40 or claim 44.

49. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 41 or claim 45.

50. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and

(ii) complements of the foregoing polynucleotides;

wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the prostate tumor protein from the sample.

51. A method according to claim 50, wherein the biological sample is blood or a fraction thereof.

52. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 50.

53. A method for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of:

- (i) a polypeptide according to claim 1;
 - (ii) a polypeptide encoded by a polynucleotide comprising a sequence provided in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
 - (iii) a polynucleotide encoding a polypeptide of (i) or (ii); and/or
 - (iv) an antigen presenting cell that expresses a polypeptide of (i) or (ii);
- under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

54. An isolated T cell population, comprising T cells prepared according to the method of claim 53.

55. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 54.

56. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

- (i) a polypeptide according to claim 1;
- (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
- (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
- (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

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57. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

(i) a polypeptide according to claim 1;

(ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;

(iii) a polynucleotide encoding a polypeptide of (i) or (ii); or

(iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate;

(b) cloning at least one proliferated cell; and

(c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

58. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and

(ii) complements of the foregoing polynucleotides;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

59. A method according to claim 58, wherein the binding agent is an antibody.

60. A method according to claim 59, wherein the antibody is a monoclonal antibody.

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61. A method according to claim 58, wherein the cancer is prostate cancer.
62. A method for monitoring the progression of a cancer in a patient, comprising the steps of:
 - (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;
 - (b) detecting in the sample an amount of polypeptide that binds to the binding agent;
 - (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
 - (d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.
63. A method according to claim 62, wherein the binding agent is an antibody.
64. A method according to claim 63, wherein the antibody is a monoclonal antibody.
65. A method according to claim 62, wherein the cancer is a prostate cancer.
66. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:
 - (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;
 - (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

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(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

67. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

68. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

69. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

70. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

71. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

72. A diagnostic kit, comprising:

(a) one or more antibodies according to claim 21; and

(b) a detection reagent comprising a reporter group.

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73. A kit according to claim 72, wherein the antibodies are immobilized on a solid support.

74. A kit according to claim 73, wherein the solid support comprises nitrocellulose, latex or a plastic material.

75. A kit according to claim 72, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

76. A kit according to claim 72, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

77. An oligonucleotide comprising 10 to 40 nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotides.

78. A oligonucleotide according to claim 77, wherein the oligonucleotide comprises 10-40 nucleotides recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

79. A diagnostic kit, comprising:
 (a) an oligonucleotide according to claim 77; and
 (b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

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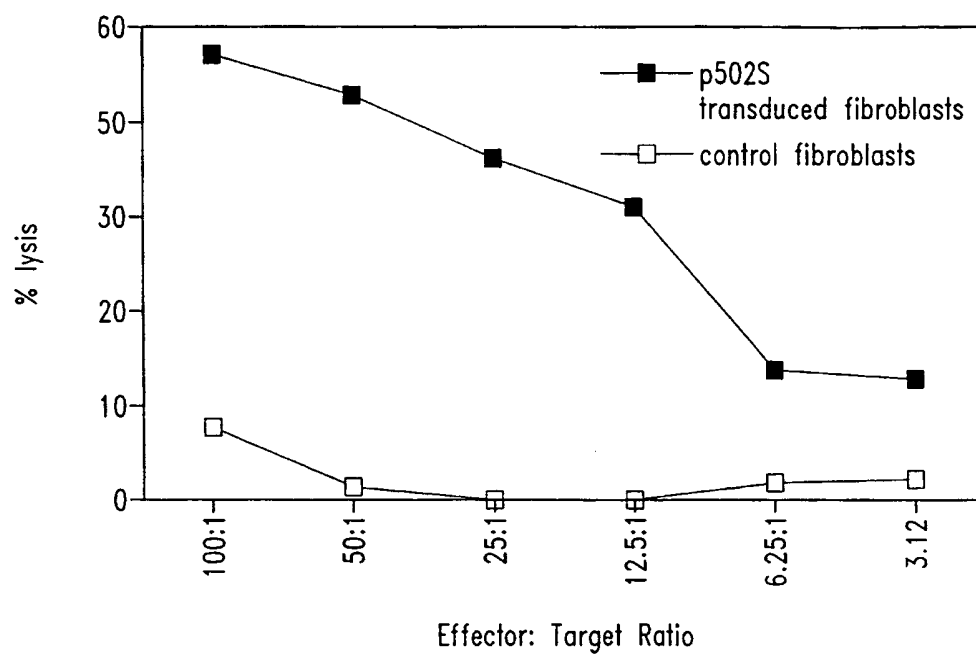


Fig. 1

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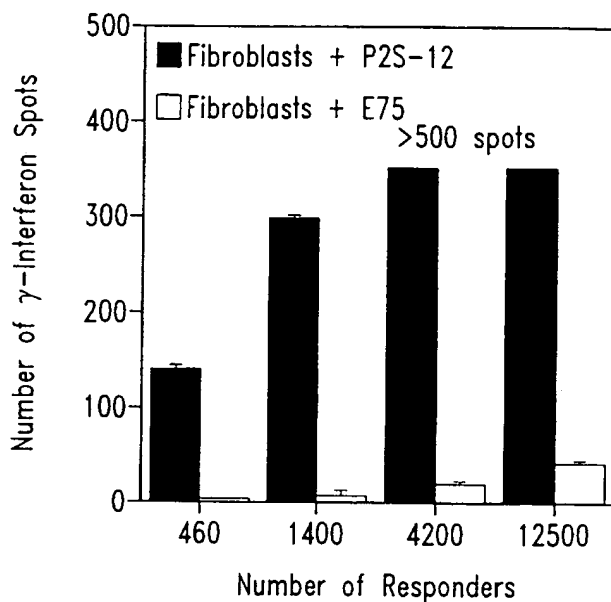


Fig. 2A

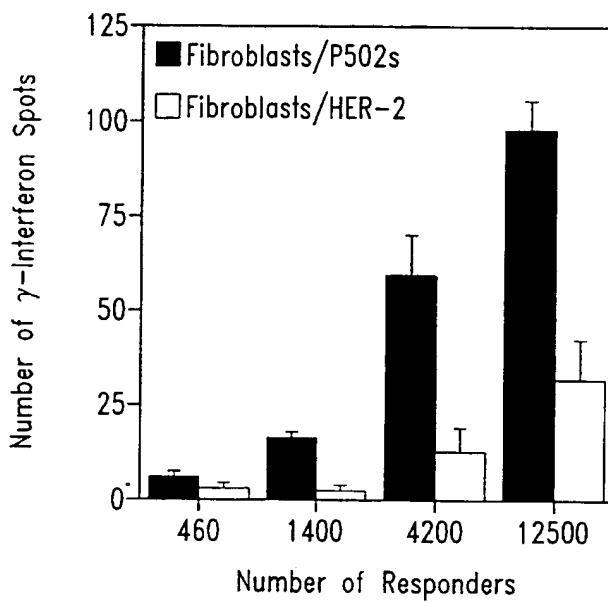


Fig. 2B

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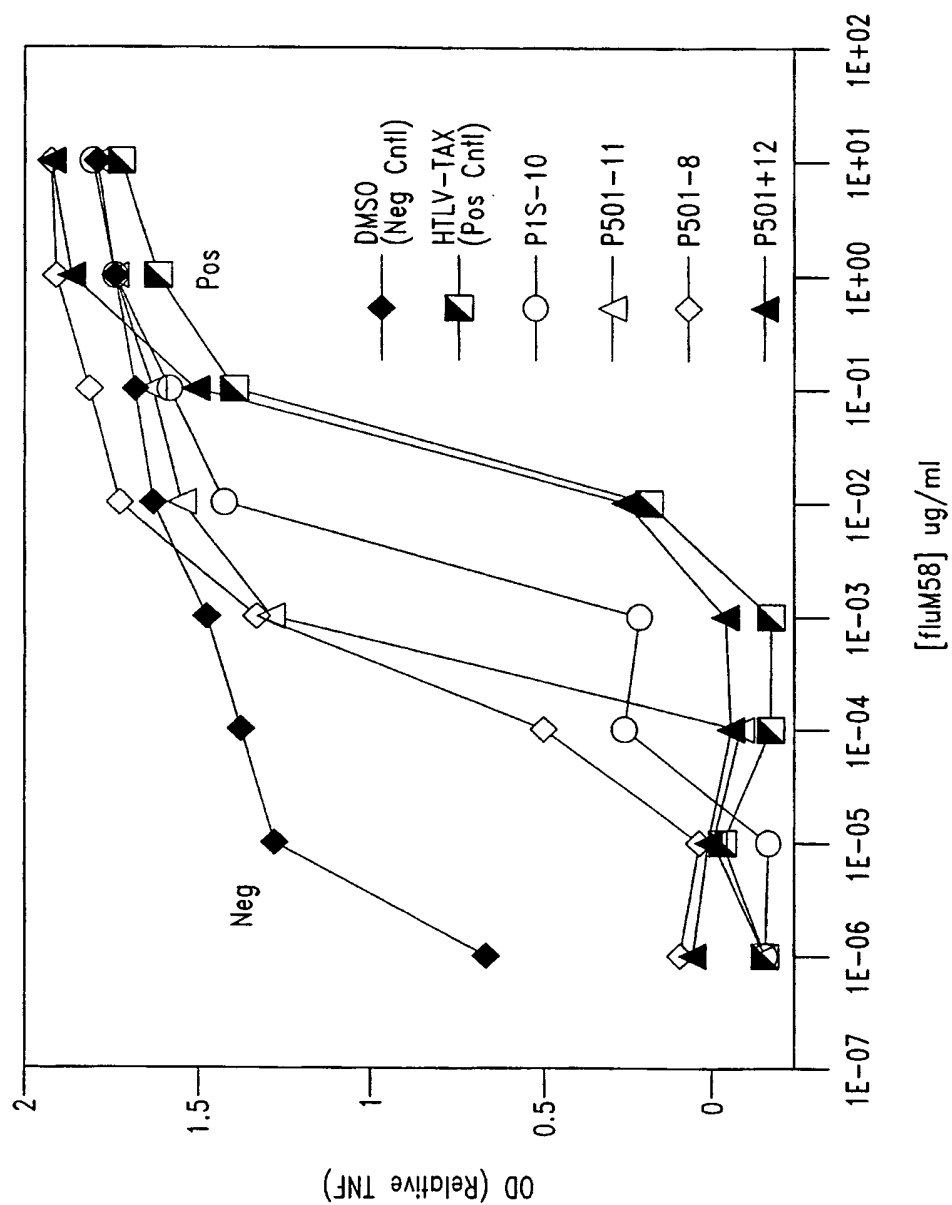


Fig. 3

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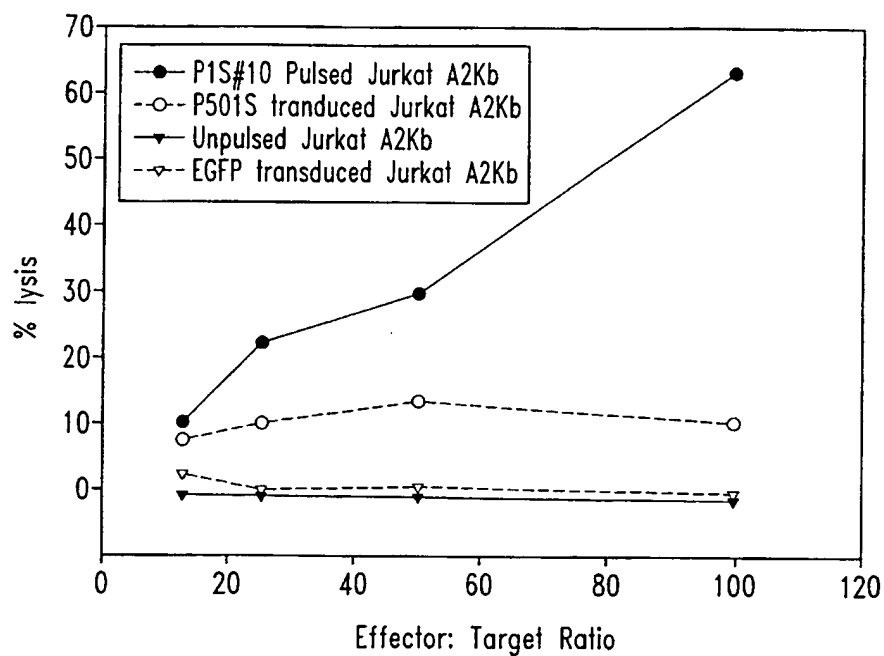


Fig. 4

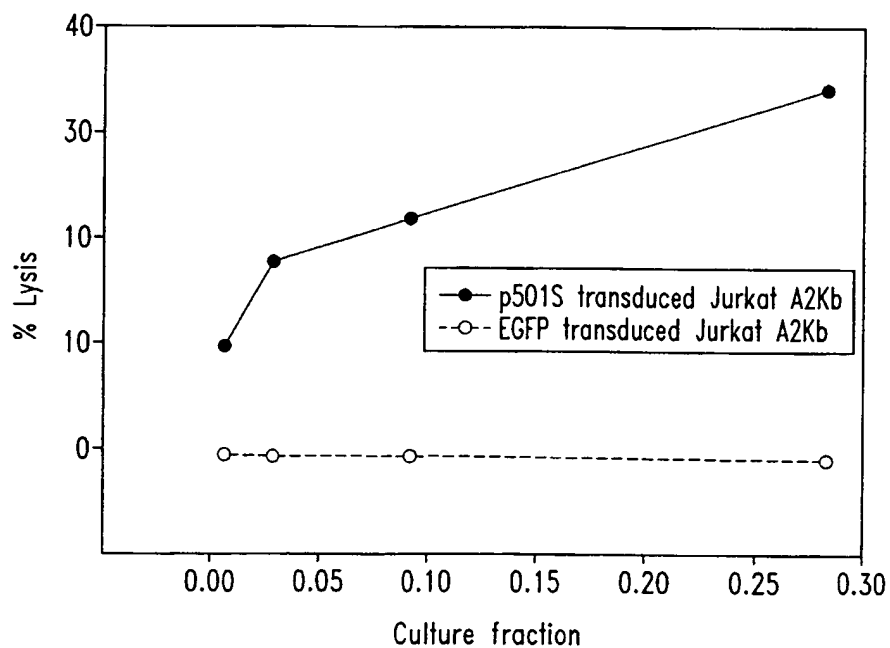


Fig. 5

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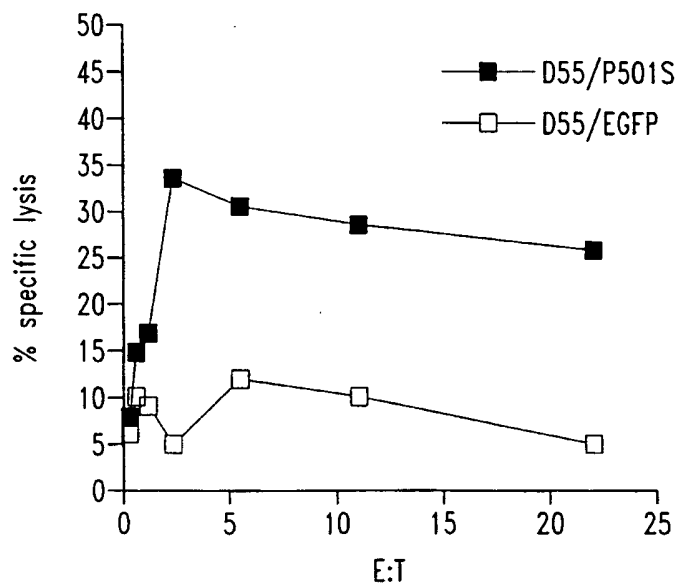


Fig. 6

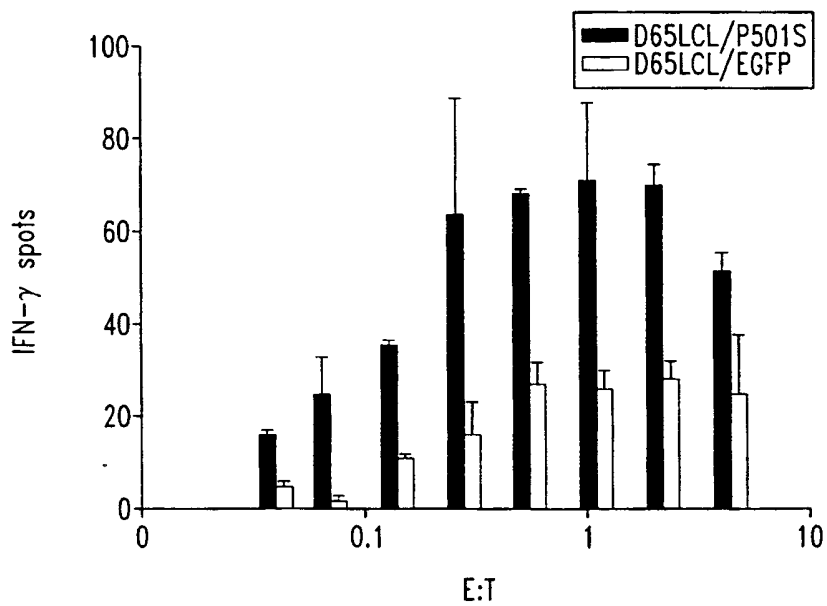


Fig. 7

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SEQUENCE LISTING

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ggcgtaatca tggcatagc tgtttcctgt gtgaaattgt tatccgctca caattcccc      540
aacatacgag ccggaacata aagtgttaag cctgggggtgc ctaatgantg agctaactcn      600
cattaattgc gttgcgtca ctgcccgtt tccagtcggg aaaactgtcg tgccactgcn      660
ttantgaatc ngccaccccc cgggaaaagg cgggttgcnt ttgggcctct tccgctttcc      720
tcgctcattg atcctngcnc ccggtcttcg gctgcggnga acggttcact cctcaaaggc      780
ggtnntccgg ttatcccaa acnggggata cccnga                                816

```

<210> 3

<211> 773

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(773)

<223> n = A,T,C or G

<400> 3

```

cttttgaaag aagggtggc tgggtgttt aacagcagag gtgcagggcg ggggtcacg      60
tctgtctct cactgggat aaacgagccc cgttccttgt tgtgatcatg atgaacaacc      120
tctcaaaag tcagaaccgg agtcacacag gcctctgtgc cgtcaaagat ttgacaccac      180
tctgccttcg tcttcttgc aaatacatct gcaaacttct tcttcatttc tggccaatca      240
tccatgctca tctgattggg aagttcatca gactttagtc canntccttt gatcagcagc      300
tcgtagaact ggggttctat tgctccaaca gccatgaatt ccccatctgc tgtcctgtaa      360
gtcgtataga aagggtgctc accatccaac atgttctgtc ctcgaggggg ggcccggtag      420
ccaattcgcc ctatantgag tctgattacg cgcgctcact ggccgtcgtt ttacaacgtc      480
gtgactggga aaaccctggg cgttaccaac ttaatcgcc tgcagcacat cccctttcg      540
ccagctgggc gtaatanca aaaggccgc accgatcgcc ctccaacag ttgcgcacct      600
gaatgggnaa atgggacccc cctgttacgg cgcattnaac ccccgnggg tttngttgtt      660
acccccacnt nnaccgctta cactttgcca gcgccttanc gcccgtccc tttcnccttt      720
cttcccttcc tttcncncn ctttccccg gggtttcccc cntcaaacc cna                                773

```

<210> 4

<211> 828

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(828)

<223> n = A,T,C or G

<400> 4

```

cctcctgagt cctactgacc tgtgctttct ggtgtggagt ccagggtctg taggaaaagg      60
aatgggcaga cacaggtgta tgccaatgtt tctgaaatgg gtataatttc gtcctctcct      120
tcggaaact ggctgtctct gaagacttct cgctcagttt cagtgaggac acacacaaag      180
acgtgggtga ccatgttgtt tgtgggtgac agagatggga ggggtggggc ccaccctgga      240
agagtggaca gtgacacaag gtggacactc tctacagatc actgaggata agctggagcc      300
acaatgcatg aggcacacac acagcaagga tgacnctgta aacatagccc acgctgtcct      360

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3

```

gngggcactg ggaagcctan atnaggccgt gagcanaaag aaggggagga tccactagtt      420
ctanagcggc cgccaccgcg gtgganctcc ancttttgtt cccttttagtg agggttaatt      480
gcgcgcttgg cntaatcatg gtcatanctn tttcctgtgt gaaattgtta tccgctcaca      540
attccacaca acatacganc cggaacata aantgtaaac ctgggggtgcc taatgantga      600
ctaactcaca ttaattgctg tgcgctcact gcccgctttc caatcnggaa acctgtcttg      660
ccncttgcac tnatgaatcn gccaaccccc ggggaaaagc gtttgcgttt tgggcgctct      720
tccgcttctc cncctcantta ntccctncnc tccgctcatc cggctgcngc aaaccgggtc      780
accnctcca aaggggggtat tccggtttcc ccnaatccgg gganancc      828

```

```

<210> 5
<211> 834
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(834)
<223> n = A,T,C or G

```

```

<400> 5
tttttttttt tttttactga tagatggaat ttattaagct tttcacatgt gatagcacat      60
agttttaatt gcatccaaag tactaacaaa aactctagca atcaagaatg gcagcatgtt      120
attttataac aatcaacacc tgtggctttt aaaatttggg tttcataaga taattttatac      180
tgaagtataa cttagccatgc ttttaaaaaa tgctttaggc cactccaagc ttggcagtta      240
acatttggca taaacaataa taaaacaatc acaatttaat aaataacaaa tacaacattg      300
taggccataa tcatatacag tataaggaaa aggtggtagt gttgagtaag cagttattag      360
aatagaatac cttggcctct atgcaaatat gtctagacac tttgattcac tcagccctga      420
cattcagttt tcaaagtagg agacagggtc tacagtatca ttttacagtt tccaacacat      480
tgaaaacaag tagaaaatga tgagttgatt tttattaatg cattacatcc tcaagagtta      540
tcaccaaccc ctcagttata aaaaattttc aagttatatt agtcatataa cttgggtgtgc      600
ttatttttaa ttagtgttaa atggattaag tgaagacaac aatgggtccc taatgtgatt      660
gatattggtc atttttacca gcttctaaat ctnaactttc aggcttttga actggaacat      720
tgnatnacag tgttccanag ttncaaccta ctggaacatt acagtgtgct tgattcaaaa      780
tgttattttg ttaaaaatta aattttaacc tgggtggaaaa ataatttgaa atna      834

```

```

<210> 6
<211> 818
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(818)
<223> n = A,T,C or G

```

```

<400> 6
tttttttttt tttttttttt aagaccctca tcaatagatg gagacatata gaaatagtca      60
aaccacatct acaaaatgcc agtatcaggg ggcggcttcg aagccaaagt gatgtttgga      120
tgtaaagtga aatattagtt ggcggatgaa gcagatagtg aggaaagtgt agccaataat      180
gacgtgaagt ccgtggaagc ctgtggctac aaaaaatgtt gagccgtaga tgccgtcgga      240
aatgggtgaag ggagactcga agtactctga ggcttgtagg agggtaaaat agagaccag      300
taaaattgta ataagcagtg ctggaattat ttggtttcgg ttgttttcta ttagactatg      360
gtgagctcag gtgattgata ctccctgatg gagtaatacg gatgtgttta ggagtgggac      420
ttctagggga tttagcgggg tgatgcctgt tggggggccg tgccctccta gttggggggt      480
aggggctagg ctggagtggg aaaaggctca gaaaaatcct gcgaagaaaa aaacttctga      540

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4

```

ggtaataaat aggattatcc cgtatcgaag gccttttttg acaggtggtg tgtggtggcc 600
ttggtatgtg ctttctcgtg ttacatcgcg ccatcattgg tatatgggta gtgtgttggg 660
ttantangg cttantatgaa gaacttttgg antggaatta aatcaatngc ttggccggaa 720
gtcattanga nggctnaaaa ggccctgtta ngggtctggg ctnggtttta cccnaccat 780
ggaatncncc ccccggaacna ntgnatccct attcttaa 818

```

<210> 7

<211> 817

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (817)

<223> n = A,T,C or G

<400> 7

```

tttttttttt tttttttttt tggctctaga ggggtagag ggggtgctat agggtaaata 60
cgggccctat ttcaaagatt tttaggggaa ttaattctag gacgatgggt atgaaactgt 120
ggtttgctcc acagatttca gagcattgac cgtagtatac ccccggtcgt gttagcggta 180
aagtggtttg gtttagacgt ccgggaattg catctgtttt taagcctaata gtggggacag 240
ctcatgagtg caagacgtct tgtgatgtaa ttattatacn aatgggggct tcaatcggga 300
gtactactcg attgtcaacg tcaaggagtc gcaggtcgcc tgggtctagg aataatgggg 360
gaagtatgta ggaattgaag attaatccgc cgtagtcggt gttctcctag gttcaatacc 420
attggtggcc aattgatttg atggtaaggg gagggatcgt tgaactcgtc tgttatgtaa 480
aggatncctt ngggatggga aggcnatnaa ggactangga tnaatggcgg gcangataatt 540
tcaaacngtc tctanttcct gaaacgtctg aaatgttaat aanaattaan tttngttatt 600
gaatnttnng gaaaagggtc tacaggacta gaaaccaaata angaaaanta atnntaangg 660
cnttatcntn aaaggtnata accnctccta tnatccacc caatngnatt cccacnccn 720
acnattggat nccccanttc canaaanggc cccccccgg tgnannccnc cttttgttcc 780
cttnantgan ggttattcnc cctngcntt atcanc 817

```

<210> 8

<211> 799

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)... (799)

<223> n = A,T,C or G

<400> 8

```

catttccggg tttactttct aaggaaagcc gagcggaagc tgctaacgtg ggaatcggtg 60
cataaggaga actttctgct ggcacgcgct agggacaagc gggagagcga ctccgagcgt 120
ctgaagcgca cgtcccagaa ggtggacttg gcaactgaaac agctgggaca catccgcgag 180
tacgaacagc gcctgaaagt gctggagcgg gaggtccagc agtgtagccg cgtcctgggg 240
tgggtggccg angcctganc cgtctgcct tgcctcccc angtgggccg ccacccctg 300
acctgacctg gtccaaacac tgagccctgc tggcggactt caagganaac cccacangg 360
ggattttgct cctanantaa ggctcatctg ggccctcgcc cccccacctg gttggccttg 420
tctttgagtg gagcccatg tccatctggg ccactgtcng gaccaccttt ngggagtgtt 480
ctccttacia ccacannatg cccggctcct cccggaaacc antccancc tngnaaggat 540
caagnctgn atccactnnt nctanaaccg gccnccnccg cngtggaacc cnccttntgt 600
tccttttctn tnagggttaa tnncccttg gccttnccan ngtcctncc nttttccnnt 660
gttnaaattg ttangcnccc nccnntccn cncnncnann cccgaccnnc annttnnann 720

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5

ncctgggggt nccnnngat tgaccenncc nccctntant tgcnttnggg nncnntgccc 780
ctttccctct nggganncg 799

<210> 9
<211> 801
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (801)
<223> n = A,T,C or G

<400> 9
acgccttgat cctcccaggc tgggactggt tctgggagga gccgggcatg ctgtggtttg 60
taangatgac actcccaaag gtggctcctga cagtggccca gatggacatg gggctcacct 120
caaggacaag gccaccaggt gcgggggccc aagcccatat gatccttact ctatgagcaa 180
aatccctgt gggggcttct ccttgaagtc cgccancagg gctcagctct tggacccang 240
caggtcatgg ggttgtnngc caactggggg ccncaacgca aaanggcncg gggcctcngn 300
caccatccc angacgcggc tacactnctg gacctccnc tccaccactt tcatgcgctg 360
ttentaccg cgnatntgtc ccantgttt cngtgcncac tccancttct nggacgtgcg 420
ctacatacgc cggantcnc nctcccgtt tgtccctatc cactgnccan caacaaattt 480
cncntantg caccnattcc cacttttnc agntttcnc nncgncttc ctntaaaaag 540
ggttganccc cggaaaatnc cccaaaaggg gggggccngg tacccaactn cccctnata 600
gctgaantcc ccatnaccnn gnetcnatgg anccntcent tttaannacn tctnaactt 660
gggaananc ctcgncntn ccccnttaa tccnccttg cnangnncnt ccccnntcc 720
ncccnntng gcntntnann cnaaaaaggc ccnnnancaa tctcctnnen cctcanttgc 780
ccanccctcg aaatcgccn c 801

<210> 10
<211> 789
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (789)
<223> n = A,T,C or G

<400> 10
cagtctatnt ggccagtgtg gcagctttcc ctgtggctgc cggtgccaca tgctgtccc 60
acagtgtggc cgtggtgaca gcttcagccg ccctcaccgg gtccaccttc tcagccctgc 120
agatcctgcc ctacacactg gcctccctct accaccggga gaagcagggt ttcttgccca 180
aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc agcttccctgc 240
caggccctaa gcctggagct cccttcctta atggacacgt ggggtgctgga ggcagtggcc 300
tgctcccacc tccaccgcg ctctgcgggg cctctgcctg tgatgtctcc gtacgtgtgg 360
tggtgggtga gccaccgan gccagggtgg ttccggggcg gggcatctgc ctggacctgc 420
ccatcctgga tagtgcttcc tgctgtccca ngtgggccca tccctgttta tgggtccat 480
tgtccagctc agccagtctg tcaactgccta tatggtgtct gccgcaggcc tgggtctggt 540
cccatttact ttgctacaca ggtantattt gacaagaacg anttgccaa atactcagcg 600
ttaaaaaatt ccagcaacat tgggggtgga aggcctgcct cactgggtcc aactccccgc 660
tctgttaac cccatggggc tgccggcttg gccgccaatt tctgttgctg ccaaantnat 720
gtggctctct gctgccacct gttgctggct gaagtgcnta cngcncanct nggggggtng 780
ggngttccc 789

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6

<210> 11
 <211> 772
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(772)
 <223> n = A,T,C or G

<400> 11
 cccaccctac ccaaataatta gacaccaaca cagaaaagct agcaatggat tcccttctac 60
 tttgttaaata aaataagtta aatatttaaa tgcctgtgtc tctgtgatgg caacagaagg 120
 accaacaggc cacatcctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc 180
 tgtgggctga ggggacctgg ttcttgtgtg ttgcccctca ggactcttcc cctacaaata 240
 actttcatat gttcaaatacc catggaggag tgtttcatcc tagaaactcc catgcaagag 300
 ctacattaaa cgaagctgca ggtaaggagg cttanagatg ggaaaccagg tgactgagtt 360
 tattcagctc ccaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc 420
 ctgagcctgg gtaatccacc tgcagagtcc ccgcattcca gtgcatggaa cccttctggc 480
 ctccctgtat aagtccagac tgaaaccccc ttggaaggnc tccagtcagg cagccctana 540
 aactggggaa aaaagaaaag gacgccccan cccccagctg tgcantctac cacctcaaca 600
 gcacagggtg gcagcaaaaa aaccacttta ctttggcaca aacaaaaact ngggggggca 660
 accccggcac cccnangggg gttaacagga ancngggnaa cntggaacct aatnaggca 720
 ggccnccac ccnaatntt gctgggaaat ttttctctcc ctaaatntt tc 772

<210> 12
 <211> 751
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(751)
 <223> n = A,T,C or G

<400> 12
 gcccgaattc cagctgccac accaccacag gtgactgcat tagttcggat gtcatacaaa 60
 agctgattga agcaaccctc tacttttttg tgcgtgagcct tttgcttggg gcaggtttca 120
 ttggctgtgt tggtagcgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg 180
 aagtanggtg agtcctcaaa atccgtatag ttggtgaagc cacagcactt gagccctttc 240
 atggtggtgt tccacacttg agtgaagtct tcctgggaac cataatcttt cttgatggca 300
 ggcactacca gcaacgtcag ggaagtgtc agccattgtg gtgtacacca aggcgaccac 360
 agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tcncgagggc 420
 acacttgtc tcagtcttan caccatanca gcccntgaaa accaananca aagaccacna 480
 cnccggctgc gatgaagaaa tnacccncg ttgacaaact tgcattggcag tggganccac 540
 agtggccna aaaatcttca aaaaggatgc ccatcnatt gaccccccaa atgcccactg 600
 ccaacagggg ctgcccacn cncnnaacga tganccnatt gnacaagatc tncntggtct 660
 tnatnaacnt gaacctgcn tngtggctcc tgttcaggnc cnggacctga cttctnaann 720
 aangaactcn gaagnccca cngganann g 751

<210> 13
 <211> 729
 <212> DNA
 <213> Homo sapien

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<220>
 <221> misc_feature
 <222> (1)...(729)
 <223> n = A,T,C or G

<400> 13
 gagccaggcg tccctctgcc tgcccactca gtggcaacac ccgggagctg ttttgtcctt 60
 tgtggancct cagcagtncc ctctttcaga actcantgcc aagancctg aacaggagcc 120
 accatgcagt gcttcagctt cattaagacc atgatgatcc tcttcaattt gtcctctttt 180
 ctgtgtgggtg cagccctggt ggcaagtgggc atctgggtgt caatcgatgg ggcacccctt 240
 ctgaagatct tcgggccact gtcgtccagt gccatgcagt ttgtcaacgt gggctacttc 300
 ctcatcgag cgggcgttgt ggtcttagct ctaggtttcc tgggctgcta tgggtgctaag 360
 actgagagca agtgtgccct cgtgacgttc ttcttcatcc tctctctcat ctctattgct 420
 gaggttgcaa tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttcttgacgt 480
 tgctggtaat gcctgccatc aanaaaagat tatgggttcc caggaanact tcaactcaagt 540
 gttggaacac caccatgaaa gggctcaagt gctgtggctt cnnccaacta tacggatttt 600
 gaagantcac ctacttcaaa gaaaanagtg cctttccccc atttctgttg caattgacaa 660
 acgtcccaa cacagccaat tgaaaacctg caccacaacc aaanggggtcc ccaaccanaa 720
 attnaaggg 729

<210> 14
 <211> 816
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(816)
 <223> n = A,T,C or G

<400> 14
 tgctcttctt caaagttggt cttgttgcca taacaaccac cataggtaaa gcgggagcag 60
 tgttcgctga aggggttgta gtaccagcgc gggatgctct ccttgacagag tcctgtgtct 120
 ggcagggtcca cgcagtgcc tttgtcactg gggaaatgga tgcgctggag ctctgcaaaag 180
 ccactcgtgt atttttcaca ggcagcctcg tccgacgcgt cggggcagtt gggggtgtct 240
 tcacactcca ggaaactgtc natgcagcag ccattgctgc agcggaaactg ggtgggctga 300
 cangtgccag agcacactgg atggcgccctt tccatgnnan gggccctgng ggaaagtccc 360
 tgancccan anctgcctct caaangcccc accttgacac ccccgacagg ctagaatgga 420
 atcttcttcc cgaaaggtag ttnttcttgt tgcccancnc ancccntaa acaaactctt 480
 gcanatctgc tccngggggg tcntantacc ancggtggaa aagaacccca ggcngcgaac 540
 caancttggt tggatncgaa gcnataatct nctnttctgc ttggtggaca gcaccantna 600
 ctgtnnanct ttagnccntg gtccctntgg gttgnncttg aacctaactn ccnntcaact 660
 gggacaaggt aantngccnt cctttnaatt cccnancntn cccctggtt tgggggtttt 720
 cncnctccta cccagaaan nccgtgttcc ccccaacta ggggccnaaa ccnnttnttc 780
 cacaaccctn cccacccac gggttcngnt ggttng 816

<210> 15
 <211> 783
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(783)
 <223> n = A,T,C or G

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<400> 15

ccaaggcctg	ggcaggcata	nacttgaagg	tacaacccca	ggaacccctg	gtgctgaagg	60
atgtggaaaa	cacagattgg	cgcctactgc	ggggtgacac	ggatgtcagg	gtagagagga	120
aagacccaaa	ccaggtggaa	ctgtggggac	tcaaggaang	cacctacctg	ttccagctga	180
cagtgactag	ctcagaccac	ccagaggaca	cggccaacgt	cacagtcact	gtgctgtcca	240
ccaagcagac	agaagactac	tgcttcgcat	ccaacaangt	gggtcgctgc	cggggctctt	300
tcccacgctg	gtactatgac	cccacggagc	agatctgcaa	gagtttcgtt	tatggaggct	360
gcttgggcaa	caagaacaac	taccttcggg	aagaagagtg	cattctancc	tgtcnggggtg	420
tgcaagggtg	gcctttgana	ngcanctctg	gggctcangc	gactttcccc	cagggccccc	480
ccatggaaag	gcgccatcca	ntgttctctg	gcacctgtca	gcccacccag	ttccgctgca	540
ncaatggctg	ctgcatcnac	antttcctng	aattgtgaca	acacccccca	ntgcccccaa	600
ccctcccaac	aaagcttccc	tgtnnaaaaa	tacnccantt	ggcttttnac	aaacnccggg	660
cncctccntt	ttcccccnnn	aaacaaagggc	netngcnttt	gaactgccc	aaccnnggaa	720
tctnccnngg	aaaaantncc	ccccctggtt	cctnnaancc	cctccnnaa	antncccccc	780
ccc						783

<210> 16

<211> 801

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (801)

<223> n = A,T,C or G

<400> 16

gccccaatte	cagctgccac	accacccacg	gtgactgcat	tagttcggat	gtcatataaaa	60
agctgattga	agcaaccctc	tacttttttg	tcgtgagcct	tttgcttggt	gcaggtttca	120
ttggctgtgt	tggtgacgtt	gtcattgcaa	cagaatgggg	gaaaggcact	gttctctttg	180
aagtaggggtg	agtcctcaaa	atccgtatag	ttgggtgaagc	cacagcactt	gagccctttc	240
atgggtggtgt	tccacacttg	agtgaagtct	tcctgggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtcag	gaagtgtctca	gccattgtgg	tgtacaccaa	ggcgaccaca	360
gcagctgcaa	cctcagcaat	gaagatgagg	aggaggatga	agaagaacgt	cncgagggca	420
cacttgctct	ccgtcttagc	accatagcag	cccangaaac	caagagcaaa	gaccacaacg	480
ccngctgcga	atgaaagaaa	ntaccacacgt	tgacaaactg	catggccact	ggacgacagt	540
tggccccgaan	atcttcagaa	aagggtatgcc	ccatcgattg	aacaccana	tgcccactgc	600
cnacagggct	gcncncncn	gaaagaatga	gccattgaag	aaggatcntc	ntggctcttaa	660
tgaactgaaa	ccntgcatgg	tggccccctgt	tcagggtctct	tggcagtga	ttctganaaa	720
aagggaacngc	ntnagcccc	ccaaangana	aaacaccccc	gggtgttgcc	ctgaattggc	780
ggccaaggan	ccctgccccn	g				801

<210> 17

<211> 740

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (740)

<223> n = A,T,C or G

<400> 17

gtgagagcca	ggcgccctc	tgcttgccca	ctcagtggca	acacccggga	gctgttttgt	60
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9

```

cctttgtgga gcctcagcag ttccctcttt cagaactcac tgccaagagc cctgaacagg      120
agccaccatg cagtgcctca gcttcattaa gaccatgatg atcctcttca atttgctcat      180
ctttctgtgt ggtgcagccc tgttggcagt gggcatctgg gtgtcaatcg atggggcatc      240
ctttctgaag atcttcgggc cactgtcgtc cagtgccatg cagtttgta acgtgggcta      300
cttcctcatc gcagccggcg ttgtggcttt tgctcttggg ttcttgggct gctatgggtgc      360
taagacggag agcaagtgtg ccctcgtgac gttcttcttc atcctcctcc tcattctcat      420
tgctgaagtt gcagctgctg tggtcgcctt ggtgtacacc acaatggctg aaccattcct      480
gacgttgctg gtantgcctg ccataanaa agattatggg ttcccaggaa aaattcactc      540
aantntggaa caccnccatg aaaagggctc caatttctgn tggcttcccc aactataccg      600
gaattttgaa agantcnccc tacttccaaa aaaaaanant tgcctttnc cccnttctgt      660
tgcaatgaaa acntccaan acngccaatn aaaacctgcc cnnncaaaaa ggntcncaa      720
caaaaaaant nnaagggttn
                                                                                   740

```

<210> 18

<211> 802

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(802)

<223> n = A,T,C or G

<400> 18

```

ccgctgggtg cgctgggtcca gngnagccac gaagcacgtc agcatacaca gcctcaatca      60
caaggtcttc cagctgccgc acattacgca gggcaagagc ctccagcaac actgcatatg      120
ggatacactt tactttagca gccaggggtga caactgagag gtgtcgaagc ttattcttct      180
gagcctctgt tagtggagga agattccggg cttcagctaa gtagtcagcg tatgtcccat      240
aagcaaacac tgtgagcagc cggagggtag aggcaaagtc actctcagcc agctctctaa      300
cattgggcat gtccagcagt tctccaaaca cgtagacacc agnggcctcc agcacctgat      360
ggatgagtggt ggcagcgcgt gcccccttgg ccgacttggc taggagcaga aattgctcct      420
ggttctgccc tgtcaccttc acttcgcac tcatactgc actgagtgtg ggggacttgg      480
gtcaggatg tccagagacg tggttccgcc ccctcnctta atgacaccgn ccanncaacc      540
gtcggctccc gccgantgng ttcgtcgtnc ctgggtcagg gtctgctggc cnctacttgc      600
aancttcgtc nggcccatgg aattcaccnc accggaactn gtangatcca ctntttctat      660
aaccggncgc caccgcnnnt ggaactccac tcttnttnc tttacttgag gggttaaggtc      720
acccttnncc ttaccttggg ccaaaccntn ccntgtgtcg anatngtnaa tcnggnccna      780
tnccanccnc atangaagcc ng
                                                                                   802

```

<210> 19

<211> 731

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(731)

<223> n = A,T,C or G

<400> 19

```

cnaagcttcc aggtnacggg ccgcnaancc tgaccnagg tancanaang cagnncgcgg      60
gagcccaccg tcacngngng gngtctttat nggagggggc ggagccacat cnctggacnt      120
cntgacccca actcccnccc ncncantgca gtgatgagtg cagaactgaa ggtnacgtgg      180
caggaaccaa gancaaannc tgctccntc caagtcggcn nagggggcgg ggctggccac      240
gcncatccnt cnagtgtgtn aaagccccnn cctgtctact tgtttgaga acngcnngna      300

```

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```

catgcccagn gttanataac nggcngagag tnannttgcc tctcccttcc ggctgcgcan 360
cngtntgct tagnggacat aacctgacta cttactgaa cccnngaac tncnccccct 420
ccactaagct cagaacaaaa aacttcgaca ccaactcantt gtcacctgnc tgctcaagta 480
aagtgtaccc catncccaat gtntgctnga ngctctgncc tgcnttangt tcggctctgg 540
gaagacctat caattnaagc tatgtttctg actgcctctt gctccctgna acaancnacc 600
cnnCNTCCA agggggggnc ggcccccaat ccccccaacc ntnaattnan ttancccn 660
ccccnggcc cggcctttta cnancntcn nnaCngggna aaacnnngc tttncccaac 720
nnaatcncc t 731

```

<210> 20

<211> 754

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (754)

<223> n = A,T,C or G

<400> 20

```

tttttttttt tttttttttt taaaaacccc ctccattnaa tgnaaacttc cgaaattgtc 60
caacccccctc ntccaaatnn cnttttccgg gnggggggttc caaacccaan ttanntttgg 120
annttaaatt aaatnttntt tggnggnna anccnaatgt nangaaagt naaccanta 180
tnancttnaa tncctggaaa ccngtngntt caaaaaatnt ttaaccctta antccctccg 240
aaatngttna nggaaaaccc aanttctcnt aagggtgttt gaaggntnaa tnaaaanccc 300
nnccaattgt ttttngccac gcctgaatta attgnttcc gntgttttcc nttaaaanaa 360
ggnnancccc ggttantnaa tcccccnnc cccaattata ccganttttt ttngaattgg 420
gancccnccg gaattaacgg ggnnntccc tnttgggggg cnggnncccc cccntcggg 480
ggttngggnc agnccnaat tgtttaaggg tccgaaaaat cctccnaga aaaaaanctc 540
ccagntgag nntngggttt ncccccccc cangggccct ctcganagt tgggggttgg 600
ggggcctggg atttntttt cctntttnc tcccccccc ccnggganag aggttngngt 660
ttgntcnnc ggccccnccn aaganctttn ccganttnan ttaaatcnt gcctnggcga 720
agtcnttgn agggntaaan ggccccctnn cggg 754

```

<210> 21

<211> 755

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (755)

<223> n = A,T,C or G

<400> 21

```

atcancccat gacccnaac nngggaccnc tcanccggnc nnncnaccnc cgcccnatca 60
nngtnagnnc actncnttn natcaacccc cncnactac gcccnananc cnacgncta 120
nncanatncc actganngcg cgangtngan ngagaaanct nataccanag ncaccanacn 180
ccagctgtcc nanaangcct nnnatacnng nnnatccaat ntgnancctc cnaagtattn 240
nncnncanat gattttcctn anccgattac cntncccc tanccectcc cccccaaacna 300
cgaaggcnct ggncnaagg nngcgncc ccgctagntc ccenncaagt cncncccta 360
aactcanccn nattacnccg ttcntgagta tcactccccg aatctcacc tactcaactc 420
aaaaanactn gatacaaat aatncaagcc tgnattatnac actntgactg ggtctctatt 480
ttagnngtcc ntnaancntc ctaatacttc cagctcnct tcnccaatt ccnaanggct 540
ctttcngaca gcatnttttg gttcccnntt ggggttcttan ngaattgcc ttcntngaac 600

```

```

gggctctctt tttccttcgg ttanccctggn ttcnncgggc cagttattat tteccntttt 660
aaattctntc cntttanttt tggcnttcna aacccccggc cttgaaaacg gccccctggt 720
aaaagggtgt tttganaaaa tttttgtttt gttcc 755

```

<210> 22

<211> 849

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(849)

<223> n = A,T,C or G

<400> 22

```

tttttttttt tttttangtg tngtcgtgca ggtagaggct tactacaant gtgaanacgt 60
acgctnngan taangcgacc cgantttctag ganncnccct aaaatcanac tgtgaagatn 120
atcctgnnna cgggaanggtc accggnngat nntgctaggg tgnccnctcc cannncttn 180
cataactcng nggccctgcc caccaccttc ggcggcccg ngncggggcc cgggtcattn 240
gnnttaaccn cactnngcna ncggtttccn nccccnng acccngggcg tccggggtn 300
tctgtcttcc cctgnagncn anaaantggg ccncggncce ctttaccct nnacaagcca 360
cngcentcta nccnngccc cccctccant nngggggact gccnangct ccgttctng 420
nnaccccnnn gggtncctcg gttgtcgant cnaccgnang ccanggatc cnaaggaagg 480
tgcgttnttg gccctaccc ttcgctnccg nncacccttc ccgacnanga nccgctccc 540
cncnccgng cctcncctcg caacaccgc nctentcngt nccggnnccc cccaccgc 600
nccctcncn ngncgnancn ctcncncc gtctcannca ccccccgc ccgccaggcc 660
ntcanccacn ggnngacnng nagnccnttc gncgcgcgn gcgncnccct cgcncngaa 720
ctnctcngg ccantnncgc tcaanccna cnaaacgcc ctgcgcggcc cgnagcgncc 780
ncctcncga gtcctcccgn cttecnacce angnttccn cgaggacacn nnaccccgcc 840
nncangcgg 849

```

<210> 23

<211> 872

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(872)

<223> n = A,T,C or G

<400> 23

```

gcgcaaaacta tacttcgctc gnactcgtgc gcctcgtcnc tcttttcttc cgcaaccatg 60
tctgacnanc ccgattnggc ngatatcnan aagntcganc agtccaaact gantaacaca 120
cacacnncan aganaaatcc nctgccttcc anagtanacn attgaacnng agaaccangc 180
nggcgaatcg taatnaggcg tgcgcgcgca atntgtcncc gtttatntn ccagctcnc 240
ctnccnacce tacntcttcn nagctgtcnn accctngtn cgnaccccc naggtcggga 300
tcgggttttn nntgaccgng cncnccctcc cccntccat nacganccn ccgcaccacc 360
nanngcncgc nccccgnct cttegcnc ccgtcctntn cccctgtngc ctggcncngn 420
accgattga ccctcgccnn ctncnngaaa ncgnanacgt ccgggttggn annancgctg 480
tggnnnngcg tctgcncgc gttccttcn ncncttcca ccatcttct tacngggtct 540
ccncgcctc tcnncacnc cctgggacgc tntcctntgc ccccttnac tccccctt 600
cgncgtgncc cgnccccacc ntcatttnc naagntcttc acaannncc ggntnnctcc 660
cnancnncn gtcancnag ggaagggng ggnnccntg nttgacgtg ngngangtc 720
cgaanantcc tcnctcan cctaccct cgggcgnct ctngttnc aacttancaa 780

```

```

ntctcccccg ngngcncttc tcagcctenc ccccccnct ctctgcantg tntcttcttc 840
tnaccnntac gantnttcgn cncctctttt cc 872

```

```

<210> 24
<211> 815
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(815)
<223> n = A,T,C or G

```

```

<400> 24
gcatgcaagc ttgagtattc tatagngtca cctaaatanc ttggcntaat catggtcnta 60
nctgncttcc tgtgtcaaata gtatacnaaa tanatatgaa tctnatntga caaganngta 120
tcntncatta gtaacaantg tntgtccat cctgtcngan canattccca tnnattncgn 180
cgcattcnen gncantatn taatngggaa ntcnntnnn ncaccnncat ctatcntncc 240
gncacctgac tggagagat ggatnanttc tntnttgacc nacatgttca tcttggattn 300
aanancccc cgcnngccac cggttngnng cnagccnntc ccaagacctc ctgtggagggt 360
aacctgcgtc aganncatca aacntgggaa acccgcnnc angtnnaagt ngnnncanan 420
gatcccgccc agnnttnacc atcccttcnc agcgcacctc ttngtgcctt anagnnagc 480
gtgtccnanc cncacaacat ganacgcgcc agnccanccg caattnggca caatgtcgnc 540
gaaccccccta gggggantna tncaaanccc caggattgtc cncncangaa atccncanc 600
cccncctac ccnctttgg gacngtgacc aantcccga gtncagtcg gccngnctc 660
ccccaccggt nncntgggg ggggaanct cngnntcanc cngncgaggn ntcgnaagga 720
accggnccctn ggcgaanng ancntcnga agngccnct cgtataaccc cccctcncca 780
nccnacngnt agntcccccc cngggtnccg aangg 815

```

```

<210> 25
<211> 775
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(775)
<223> n = A,T,C or G

```

```

<400> 25
ccgagatgtc tcgctccgtg gccttagctg tgctcgcgt actctctctt tctggcctgg 60
aggctatcca gcgtactcca aagattcagg ttactcacg tcatccagca gagaatggaa 120
agtcaaattt cctgaattgc tatgtgtctg ggtttcatcc atccgacatt gaanttgact 180
tactgaagaa tgganagaga attgaaaaag tggagcattc agacttgtct ttcagcaagg 240
actggtcttt ctatctctg tactacactg aattcacccc cactgaaaaa gatgagtatg 300
cctgccgtgt gaaccatgtg actttgtcac agcccaagat agttaagtgg gatcgagaca 360
tgtaagcagn cncatggaa gttgaagat gccgcatttg gattggatga attccaaatt 420
ctgcttgctt gcnttttaaa antgatatgc ntataacccc taccctttat gncccccaaat 480
tgtaggggtt acatnantgt tcncntngga catgatcttc ctttataant cncncttcg 540
aattgcccgt cncnctgtt ngaatgtttc cnaaaccacg gttggctccc ccaggtncc 600
tcttacggaa gggcctgggc cnccttncaa ggttggggga accnaaaatt tcncttntgc 660
cncncccca cnccttngn nncncanttt ggaaccttc cnatccccc tggcctcnna 720
nccttnncta anaaaacttn aaancgtngc naaantttt acttcccccc ttacc 775

```

```

<210> 26

```

<211> 820
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(820)
 <223> n = A,T,C or G

<400> 26
 anattantac agtghtaatct tttcccagag gtgtgtanag ggaacggggc ctagaggcat 60
 cccanagata ncttatanca acagtgtctt gaccaagagc tgctgggcac atttcctgca 120
 gaaaagggtgg cgggtcccat cactcctcct ctcccatagc catcccagag gggtagtag 180
 ccatcangcc ttcggtggga gggagtcang gaaacaacan accacagagc anacagacca 240
 ntgatgacca tggggcgggag cgagcctctt ccctgnaccg gggtaggana nganagccta 300
 nctgaggggt cacactataa acgttaacga ccnagatnan cacctgtctt aagtgcaccc 360
 ttcctacctg acnaccagng accnnnaact gcngcctggg gacagcctg ggancagcta 420
 acnnagcact cacctgcccc cccatggcgg tncgctcctc tggtcctgnc aagggaagct 480
 cctgttgga attncgggga naccaaggga nccccctcct ccactgtga aggaaaaann 540
 gatggaattt tnccttccg gccnntcccc tcttcttcta cagccccct nntactctc 600
 tccctctntt nctcgtcnc acttttnacc ccnnnatttc ccttnattga tcggannctn 660
 ganattccac tnnccgtcnc cntcnatcng naanacnaaa nactntctna cccnggggat 720
 gggnnccctg ntcactctct ctttttctct accnccnntt ctttgctct ccttngatca
 780tccaacctc gntggccntn ccccccnnn tcttttccc
 820

<210> 27
 <211> 818
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(818)
 <223> n = A,T,C or G

<400> 27
 tctgggtgat ggccctcttc tctcagga cctctgactg ctctgggcca aagaatctct 60
 tgtttcttct ccgagcccca ggcagcgggtg attcagccct gcccacctg attctgatga 120
 ctgcggatgc tgtgacggac ccaaggggca aatagggtcc cagggtccag ggaggggcgc 180
 ctgctgagca ctccgcctcc tcacctgcc cagccctgc catgagctct gggctgggtc 240
 tccgcctcca gggttctgct ctccangca ngccancaa tggcgctggg ccacactggc 300
 ttcttctgct cccctcctg gctctganc tctgtcttcc tgtcctgtgc angcncctg 360
 gatctcagtt tccctcctc anngaactct gtttctgann tcttcantta actntgantt 420
 tatnaccnan tggctgtnc tgcnnactt taatgggcn gaccggctaa tccctcctc 480
 nctcccttcc anttccnnna accncttnc cntctctcc ccntancccg ccngggaanc 540
 ctcttttgc ctnaccangg gccnnnaccg cccntnctn ggggggcnng gtnnctnnc 600
 ctgntnnccc cctcncntt tncctcgtcc cncnncnng nngcannctc ncngtcccn 660
 tnnctcttct ngntcgnaa ngntcncnt tnnnnngnng ngntnntnct tccctctcnc 720
 cnnntgnang tnnnnnnnc ncngnnccc nnnncnnnn nggnntnnn tctnncngc 780
 cccnncccc ngnattaagg cctcnnctc ccggccnc 818

<210> 28
 <211> 731
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(731)

<223> n = A,T,C or G

<400> 28

aggaagggcg	gagggatatt	gtangggatt	gagggatagg	agnataangg	gggaggtgtg	60
tcccaacatg	anggtgnggt	tctcttttga	angaggggtg	ngtttttann	ccnggtgggt	120
gattnaaccc	cattgtatgg	agnnaaagg	tttnagggat	ttttcggctc	ttatcagtat	180
ntanattcct	gtnaatcggg	aaatnatntt	tcnncnggaa	aatnttgctc	ccatccgnaa	240
attnctcccg	ggtagtgcac	nttngggggn	cngccangtt	tcccaggctg	ctanaatcgt	300
actaaagntt	naagtgggan	tncaaataaa	aacctnncac	agagnatccn	tacccgactg	360
tnnnntnctt	tgcctctntg	actctgcnn	agcccaatac	ccnngngnat	gtcncccnng	420
nnngcgcnc	tgaaannnnc	tcgnggctnn	gancatcang	gggtttcgca	tcaaaagcnn	480
cgtttctcat	naaggcactt	tngcctcatc	caaccnctng	ccctcnncca	tttngccgtc	540
nggttcnctt	acgctnnntg	cncctnnntn	ganattttnc	ccgcctnggg	naancctcct	600
gnaatgggta	gggncttntc	ttttnacnnc	gnggtntact	aatcnnctnc	acgctnctt	660
tctcnacccc	cccccttttt	caatcccanc	ggcnaatggg	gtctccccnn	cgangggggg	720
nnnccannnc	c					731

<210> 29

<211> 822

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(822)

<223> n = A,T,C or G

<400> 29

actagtccag	tgtgggtggg	ttccattgtg	ttggggncnc	ttctatgant	antnttagat	60
cgctcanacc	tcacancctc	ccnancngc	ctataangaa	nannaataga	nctgtncnnt	120
atntntacnc	tcatanncct	cnnnaccac	tcctctctaa	ccctactgtg	gcctatngcn	180
tnnctantct	ntgccgcctn	cnanccaccn	gtggggccnac	cncnngnatt	ctcnatctcc	240
tcnccatntn	gcctananta	ngtncatacc	ctatacctac	nccaatgcta	nnnctaancn	300
tccatnantt	annntaacta	ccactgaant	ngactttcnc	atnancctct	aatttgaatc	360
tactctgact	cccacngcct	annnattagc	ancntcccc	nacnatntct	caaccaaate	420
ntcaacaacc	tatctanctg	ttcnccaacc	nttncctccg	atccccnnac	aacccccctc	480
ccaaataacc	nccacctgac	ncctaaccn	caccatcccg	gcaagccnan	ggncatttan	540
ccactggaat	cacnatngga	naaaaaaaac	ccnaactctc	tancncnnat	ctccctaana	600
aatnctcctn	naatttactn	ncantnccat	caancccaen	tgaaacnnaa	ccccgttttt	660
tanatecctt	ctttcgaaaa	ccnacccttt	annncccaac	ctttngggcc	ccccnctnc	720
ccnaatgaag	gncncccaat	cnangaaacg	ncnctgaaaa	ancnaggcna	anannntccg	780
canatectat	eccttanttn	ggggnccttt	nccnngggcc	cc		822

<210> 30

<211> 787

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(787)

<223> n = A,T,C or G

<400> 30

cggccgcctg	ctctggcaca	tgcctcctga	atggcatcaa	aagtgatgga	ctgcccattg	60
ctagagaaga	ccttctctcc	tactgtcatt	atggagccct	gcagactgag	ggctccccct	120
gtctgcagga	tttgatgtct	gaagtcgtgg	agtgtggctt	ggagctcctc	atctacatna	180
gctggaagcc	ctggagggcc	tctctcgcca	gcctccccct	tctctccacg	ctctccangg	240
acaccagggg	ctccaggcag	cccattatct	ccagnangac	atgggtgttc	tccacgcgga	300
cccatggggc	ctgnaaggcc	agggctcctt	ttgacaccat	ctctcccgtc	ctgcctggca	360
ggccgtggga	tccactantt	ctanaacggn	cgccaccncg	gtgggagctc	cagcttttgt	420
tcccnttaat	gaagggtaat	tgcncgcttg	gcgtaatcat	nggtcanaac	tntttcctgt	480
gtgaaattgt	ttntccccct	ncnatteenc	ncnacatacn	aacccggaan	cataaagtgt	540
taaagcctgg	gggtngcctn	nngaataaac	tnaactcaat	taattgcgtt	ggctcatggc	600
ccgctttccn	ttcnggaaaa	ctgtctntccc	ctgenttntt	gaatcggcca	ccccccnggg	660
aaaagcggtt	tgcnttttng	ggggntcctt	ccncttcccc	cctcncctaan	ccctncgcct	720
cggtcgttnc	nggtngcggg	gaangggnat	nnctccccnc	naagggggng	agnnnngtat	780
ccccaaa						787

<210> 31

<211> 799

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(799)

<223> n = A,T,C or G

<400> 31

tttttttttt	ttttttttgg	gatgctactg	tttaattgca	ggaggtgggg	gtgtgtgtac	60
catgtaccag	ggctattaga	agcaagaagg	aaggaggagg	ggcagagcgc	cctgctgagc	120
aacaaaggac	tcttcgagcc	ttctctgtct	gtctcttggc	gcaggcacat	ggggaggcct	180
cccgaggggt	ggggggccacc	agtccagggg	tgggagcact	acanggggtg	ggagtgggtg	240
gtggctggtn	cnaatggcct	gncacanatc	cctacgatct	ttgacacctg	gatttcacca	300
ggggaccttc	tgtttcctca	nggnaacttc	ntnnatctcn	aaagaacaca	actgtttctt	360
cngcanttct	ggctgttcat	ggaaagcaca	gggtgtccnat	ttnggctggg	acttgggtaca	420
tatggttccg	gcccacctct	ccntcnaaan	aagtaattca	cccccccccn	ccntctnttg	480
cctgggcctt	taantacceca	caccggaact	canttantta	ttcatcttng	gntgggcttg	540
ntnatcncn	cctgaangcg	ccaagttgaa	aggccacgcc	gtncnccnctc	cccatagnan	600
nttttnncnt	canctaatagc	ccccccnggc	aacnatccaa	tcccccccn	tgggggcccc	660
agccccanggc	ccccgntctg	ggnnnccngn	cncgnantcc	ccaggntctc	ccantcngnc	720
ccnnngcncc	cccgcacgca	gaacanaagg	ntngagccnc	cgcannnnnn	nggtnnncnac	780
ctcgcccccc	ccnnccgngg					799

<210> 32

<211> 789

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(789)

<223> n = A,T,C or G

```

<400> 32
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt    60
tttttccnag ggcaggttta ttgacaacct cncgggacac aancaggctg gggacaggac    120
ggcaaacaggc tccggcggcg gcggcggcgg ccctacctgc ggtaccaa atgcagcctc    180
cgctcccget tgatnttcc tgcagctgc aggatgcctt aaaacagggc ctccggcctn    240
ggtgggcacc ctgggatttn aatttccacg ggcacaatgc ggtcgcancc cctcaccacc    300
nattaggaat agtggnttta ccncncnccg ttggcncact cccntggaa accacttntc    360
gcggctccgg catctggtct taaaccttgc aaacnctggg gccctctttt tggttantnt    420
nccngccaca atcatnactc agactggcnc gggctggccc caaaaaancn ccccaaaacc    480
ggnccatgtc ttncgggggt tgctgcnatn tncatcacct cccgggcnca ncaggncaac    540
ccaaagttc ttngggcccn caaaaaancn ccggggggnc ccagtttcaa caaagtcac    600
ccccttggcc cccaaatcct ccccccgnnt nctgggtttg ggaacccacg cctctnnctt    660
tggngggcaa gntggntccc ccttcggggc cccggtgggc ccnctctaa ngaaaacncc    720
ntcctnnnca ccaccccc nngnnacgnc tancaangna tcctttttt tanaaacggg    780
ccccccnccg                                     789

```

<210> 33

<211> 793

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(793)

<223> n = A,T,C or G

```

<400> 33
gacagaacat gttggatggt ggagcacctt tctatacgac ttacaggaca gcagatgggg    60
aattcatggc tgttggagca atanaacccc agttctacga gctgctgac aaaggacttg    120
gactaaagtc tgatgaactt cccaatcaga tgagcatgga tgattggcca gaaatgaana    180
agaagtttgc agatgtattt gcaaagaaga cgaaggcaga gtggtgtcaa atctttgacg    240
gcacagatgc ctgtgtgact ccggttctga cttttgagga ggttgttcat catgatcaca    300
acaangaacg gggctcgttt atcaccantg aggagcagga cgtgagcccc cgccctgcac    360
ctctgctgtt aaacaccccc gccatccctt ctttcaaaag ggatccacta cttctagagc    420
ggncgccacc gcggtggagc tccagctttt gttcccttta gtgagggtta attgcgcgct    480
tggcgtaatc atggtcatan ctgtttcctg tgtgaaattg ttatccgctc acaattccac    540
acaacatacg anccggaagc atnaaathtt aaagcctggn ggtngcctaa tgantgaact    600
nactcacatt aattggcttt gcgctcactg cccgctttcc agtccggaaa acctgtcctt    660
gccagctgcc nttaatgaat cnggccaccc cccggggaaa aggcngtttg cttnttgggg    720
cgcncctccc gctttctcgc ttcttgaant cttccccccc ggtctttcgg cttgcggcna    780
acggtatcna cct                                     793

```

<210> 34

<211> 756

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(756)

<223> n = A,T,C or G

```

<400> 34
gccgcgaccg gcatgtacga gcaactcaag ggcgagtggg accgtaaaag ccccaatctt    60
ancaagtgcg gggaanagct gggtcgactc aagctagtct ttctggagct caacttcttg    120

```

ccaaccacag	ggaccaagct	gaccaaacag	cagctaattc	tggcccgtga	catactggag	180
atcggggccc	aatggagcat	cctacgcaan	gacatcccc	ccttcgagcg	ctacatggcc	240
cagctcaa	gctactactt	tgattacaan	gagcagctcc	ccgagtcagc	ctatatgcac	300
cagctcttgg	gcctcaacct	cctcttctctg	ctgtcccaga	accgggtggc	tgantnccac	360
acgganttgg	ancggctgcc	tgcccaanga	catacanacc	aatgtctaca	tcnaccacca	420
gtgtccttga	gcaataactga	tgganggcag	ctaccncaaa	gtnttcctgg	ccnagggtaa	480
catccccgcg	cgagagctac	accttcttca	ttgacatcct	gctcgacact	atcagggatg	540
aaaatcgeng	ggttgctcca	gaaaggctnc	aanaanatcc	ttttcncctga	aggcccccg	600
atnncctagt	nctagaatcg	gcccggccatc	gcggtgganc	ctccaacctt	tcgttnccct	660
ttactgaggg	ttnattggcg	cccttggcgt	tatcatggtc	acnccngttn	cctgtgttga	720
aattnttaac	ccccacaa	tccacgccna	cattng			756

<210> 35
 <211> 834
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (834)
 <223> n = A,T,C or G

<400> 35						
ggggatctct	anatchacct	gnatgcatgg	ttgtcgggtg	ggtcgctgtc	gatgaanatg	60
aacaggatct	tgcccttgaa	gctctcggct	gctgtnttta	agttgctcag	tctgccgtca	120
tagtcagaca	cncctctggg	caaaaaacan	caggatntga	gtcttgattt	cacctccaat	180
aatcttcngg	gctgtctgct	cggtgaactc	gatgacnang	ggcagctgg	tgtgtntgat	240
aaantccanc	angttctcct	tggtgacctc	cccttcaaag	ttgttccggc	cttcatcaaa	300
cttctnnaan	angannancc	canctttgtc	gagctggnat	ttgganaaca	cgtcacctgt	360
ggaaactgat	cccaaaggt	atgtcatcca	tgcctctgc	tgcctgcaaa	aaacttgctt	420
ggcncaaatac	cgactcccn	tccttgaaag	aagccnatca	cacccccctc	cctggactcc	480
nncaangact	ctnccgctnc	ccntccnng	cagggttggt	ggcannccgg	gccccngcgc	540
ttcttcagcc	agttcacnat	nttcatcagc	ccctctgcca	gctgtnttat	tccttggggg	600
ggaanccgtc	tctcccttcc	tgaannaact	ttgaccgtng	gaatagccgc	gcntcncnt	660
acntnctggg	ccgggttcaa	antccctccn	ttgncnntcn	cctcggggcca	ttctggattt	720
nccnaacttt	ttccttcccc	cncctcncgg	ngtttggnnt	tttcatnggg	ccccaaactct	780
gctnttgccc	antcccttgg	gggcntntan	cncctcctnt	ggccccntng	ggcc	834

<210> 36
 <211> 814
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (814)
 <223> n = A,T,C or G

<400> 36						
cggnccgttt	ccngccgcgc	cccgtttcca	tgacnaaggc	tcctttcang	ttaaatacnn	60
cctagnaaac	attaatgggt	tgctctacta	atacatcata	cnaaccagta	agcctgcccc	120
naacgccaac	tcaggccatt	cctaccaaag	gaagaaaggc	tggtctctcc	acccccgtga	180
ggaaaggcct	gccttgtaag	acaccacaat	ncggctgaat	ctnaagtctt	gtgttttact	240
aatggaaaaa	aaaaataaac	aanaggtttt	gttctctatg	ctgcccaccg	cagcctggca	300
ctaaaacanc	ccagcgctca	cttctgcttg	ganaaatatt	ctttgctctt	ttggacatca	360

```

ggcttgatgg tatcactgcc acntttccac ccagctgggc ncccttcccc catntttgtc 420
antganctgg aaggcctgaa ncttagtctc caaaagtctc ngcccacaag accggccacc 480
aggggagtc ntttncagtg gatctgcca anantaccn tatcatcnnt gaataaaaaag 540
gcccctgaac ganatgcttc cancanctt taagacccat aatcctngaa ccattggtgcc 600
cttccggtct gatecnaaag gaatgttctt ggggtccant ccctcctttg ttncttacgt 660
tgtnttggac cntgtctngn atnaccnaan tganatcccc ngaagcacc tncctctggc 720
atttganttt cntaaattct ctgccctacn nctgaaagca cnattccctn ggcncnaaan 780
ggngaactca agaaggtctn ngaaaaacca cncn 814

```

<210> 37

<211> 760

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (760)

<223> n = A,T,C or G

<400> 37

```

gcatgctgct ctccctcaaa gttgttcttg ttgccataac aaccaccata ggtaaagcgg 60
gcgcagtgtt cgctgaagg gttgtagtac cagcgcgga tgctctcctt gcagagtcct 120
gtgtctggca ggtccacgca atgcccttg tctactggga aatggatgcg ctggagctcg 180
tcnaanccac tcgtgtattt ttcacangca gcctcctccg aagcctccgg gcagttgggg 240
gtgtctgcac actccactaa actgtcgatn cancagccca ttgctgcagc ggaactgggt 300
gggctgacag gtgccagaac aactggatn ggcctttcca tgggaaggcc tgggggaaat 360
cncctnancc caaactgcct ctcaaaggcc accttgaca ccccgacagg ctagaaatgc 420
actcttcttc ccaaaggtag ttgttcttgt tgcccaagca ncctccanca aacccaaanc 480
ttgcaaaatc tgctccgtgg gggctcatnnn taccanggtt ggggaaanaa acccggcngn 540
gancncctt gtttgaatgc naaggaata atcctcctgt ctgtcttggg tggaaanagca 600
caattgaact gttaacnttg ggcgngttc cctnnggtg gtctgaaact aatcacctgc 660
actggaaaaa ggtangtgc ttccttgaat tcccaaantt cccctngntt tgggtntttt 720
ctctctncc ctaaaaatcg tnttcccccc cntanggcg 760

```

<210> 38

<211> 724

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (724)

<223> n = A,T,C or G

<400> 38

```

tttttttttt tttttttttt tttttttttt ttttttaaaa cccctccat tgaatgaaaa 60
cttcnnaaat tgtccaaccc cctcnccaa atnnccattt ccgggggggg gttccaaacc 120
caaattaatt ttgganttta aattaaatnt tnattngggg aanaanccaa atgtnaagaa 180
aatttaaccc attatnaact taaatnctn gaaaccntg gnttccaaa atttttaacc 240
cttaaatecc tccgaaattg ntaangaaa accaaattcn cctaaggctn tttgaaggtt 300
ngatttaaac ccccttnant tnttttnacc cngnctnaa ntattngnt tccggtgtt 360
tcctnttaan cntnggtaac tcccngtaat gaannncct aanccaatta aaccgaattt 420
tttttgaatt ggaaattccn ngggaattna ccggggtttt tccnttttg gggccatncc 480
ccncttttcg ggggttgggn ntagggtgaa ttttttnang ncccaaaaaa ncccccaana 540
aaaaaactcc caagnnttaa ttngaantnc ccccttccca ggcttttttg gaaagnggg 600

```

tttntggggg ccngggantt cnttcccccn ttncnccccc ccccccnggt aaanggttat	660
ngnnttttggg ttttgggccc cttnanggac cttccggatn gaaattaaat ccccggnccg	720
gccg	724

<210> 39

<211> 751

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(751)

<223> n = A,T,C or G

<400> 39

tttttttttt tttttctttg ctcacattta atttttattt tgattttttt taatgctgca	60
caacacaata tttatttcat ttgtttcttt tatttcattt tatttgtttg ctgctgctgt	120
tttatttatt tttactgaaa gtgagaggga acttttgtgg ccttttttcc tttttctgta	180
ggccgcctta agctttctaa atttggaaaca tctaagcaag ctgaanggaa aagggggttt	240
cgcaaatca ctcgggggaa nggaaagggt gctttgttaa tcatgcccta tgggtgggtga	300
ttaactgctt gtacaattac ntttcacttt taattaattg tgctnaangc ttttaattana	360
cttgggggtt ccctccccc accaaccnccn ctgacaaaaa gtgccngccc tcaaatnatg	420
tcccggcnnt cnttgaaaca cacngcngaa ngttctcatt ntcccnccn caggtnaaaa	480
tgaagggtta ccatntttaa cncacctcc acntggcnnn gcctgaatcc tcnaaaancn	540
ccctcaancn aattnctnng ccccggtcnc gcntnngtc cccccgggct ccgggaantn	600
caccccnga annnntnnc naacnaaatt ccgaaatat tccnntcnc tcaattcccc	660
cnnagactnt cctcnncnan cncaatttc ttttntcac gaacncgnnc cnnaaatgn	720
nnnnncctc cncnngtcn naatcnccan c	751

<210> 40

<211> 753

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(753)

<223> n = A,T,C or G

<400> 40

gtgggtatttt ctgtaagatc aggtgttccct ccctcgtagg tttagaggaa acaccctcat	60
agatgaaaaac ccccccgaga cagcagcact gcaactgccca agcagccggg gtaggagggg	120
cgccctatgc acagctgggc ccttgagaca gcagggttc gatgtcaggc tcgatgtcaa	180
tgggtctggaa gcggcggttg tacctgcgta ggggcacacc gtccagggcc accaggaact	240
tctcaaagtt ccaggcaacn tcgttgcgac acaccggaga ccaggatgatn agcttggggg	300
cggtcataan cgcggtggcg tcgtcgctgg gagctggcag ggcctccgc aggaaggcna	360
ataaaagggtg cgccccgca ccgttcacnt cgcacttctc naanaccatg angttgggct	420
cnaacccacc accannccgg acttccttga nggaattccc aaatctcttc gntcttgggc	480
ttctnctgat gccctanctg gttgcccnngn atgccaanca nccccaancc ccggggctcct	540
aaancaccn cctcctcntt tcatctgggt tntntcccc ggaccntggt tcctctcaag	600
ggancccata tctcnaccn tactcacnt nccccccnt gnnacccanc cttctannng	660
ttccncccg nctctggcc cntcaanan gcttnacna cctgggtctg ccttcccccc	720
tnccctatct gnaccccn nttgtctcan tnt	753

<210> 41

<211> 341
 <212> DNA
 <213> Homo sapien

<400> 41
 actatatcca tcacaacaga catgcttcat cccatagact tcttgacata gcttcaaagt 60
 agtgaaccca tccttgattt atatacatat atgttctcag tattttggga gcctttccac 120
 ttctttaaac cttgttcatt atgaacactg aaaataggaa tttgtgaaga gttaaaaagt 180
 tatagcttgt ttacgtagta agtttttgaa gtctacattc aatccagaca cttagttgag 240
 tgttaaactg tgatttttaa aaaatatcat ttgagaatat tctttcagag gtattttcat 300
 ttttactttt tgattaattg tgttttatat attagggtag t 341

<210> 42
 <211> 101
 <212> DNA
 <213> Homo sapien

<400> 42
 acttactgaa tttagtcttg tgctcttctt tatttagtgt tgtatcataa atactttgat 60
 gtttcaaaca ttctaataaa ataattttca gtggcttcat a 101

<210> 43
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 43
 acatctttgt tacagtctaa gatgtgttct taaatcacca ttccttcttg gtcctcacc 60
 tccagggtag tctcacactg taattagagc tattgaggag tctttacagc aaattaagat 120
 tcagatgcct tgctaagtct agagttctag agttatgttt cagaaagtct aagaaaccca 180
 cctcttgaga ggtcagtaaa gaggacttaa tatttcatat ctacaaaatg accacaggat 240
 tggatacaga acgagagtta tcctggataa ctgagagctg agtacctgcc cgggggcccgc 300
 tcgaa 305

<210> 44
 <211> 852
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(852)
 <223> n = A,T,C or G

<400> 44
 acataaatat cagagaaaag tagtctttga aatatttacg tccaggagtt ctttgtttct 60
 gattatttgg tgtgtgtttt gggttgtgtc caaagtattg gcagcttcag ttttcatttt 120
 ctctccatcc tcgggcattc ttcccaaatt tatataccag tcttcgtcca tccacacgct 180
 ccagaatttc tctttttag tagaatctca tagctcggct gagcttttca taggtcatgc 240
 tgctgttgtt cttcttttta ccccatagct gagccactgc ctctgatttc aagaacctga 300
 agacgccctc agatcggtct tcccatttta ttaatcctgg gttcttgtct gggttcaaga 360
 ggatgtcgcg gatgaattcc cataagtgag tccctctcgg gttgtgcttt ttgggtgtggc 420
 acttggcagg ggggtcttgc tcctttttca tatcaggtga ctctgcaaca ggaaggtgac 480
 tggtggttgt catggagatc tgagcccggc agaaaagttt gctgtccaac aaatctactg 540
 tgctaccata gttgggtgtc tataaatagt tctngtcttt ccagggtgtt atgatggaag 600

```

gctcagtttg ttcagtcttg acaatgacat tgtgtgtgga ctggaacagg tcactactgc      660
actggccggt ccacttcaga tgctgcaagt tgctgtagag gagntgcccc gccgtccrtg      720
ccgcccgggt gaactcctgc aaactcatgc tgcaaagggt ctgcccggtg atgtcgaact      780
cntggaaagg gatacaattg gcatccagct gggttggtgtc caggagggtga tggagccact      840
cccacacctg gt                                     852

```

<210> 45

<211> 234

<212> DNA

<213> Homo sapien

<400> 45

```

acaacagacc cttgctcgct aacgacctca tgctcatcaa gttggacgaa tccgtgtccg      60
agtctgacac catccggagc atcagcattg cttcgcagtg ccctaccgcg gggaaactctt      120
gcctcgtttc tggctggggg ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg      180
tgaacgtgtc ggtggtgtct gaggagggtc gcagtaagct ctatgacccg ctgt          234

```

<210> 46

<211> 590

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(590)

<223> n = A,T,C or G

<400> 46

```

actttttatt taaatgttta taaggcagat ctatgagaat gatagaaaac atggtgtgta      60
atttgatagc aatatttttg agattacaga gttttagtaa ttaccaatta cacagttaaa      120
aagaagataa tatattccaa gcanatacaa aatatctaata gaaagatcaa ggcaggaaaa      180
tgantataac taattgacaa tggaaaatca attttaatgt gaattgcaca ttatccttta      240
aaagctttca aaanaanaaa ttattgcagt ctanttaatt caaacagtgt taaatggtat      300
caggataaan aactgaaggg canaaagaat taattttcac ttcatgtaac ncacccanat      360
ttacaatggc ttaaattgcan ggaaaaagca gtggaagtag ggaagtantc aaggtctttc      420
tggctctctaa tctgccttac tctttgggtg tggctttgat cctctggaga cagctgccag      480
ggctcctgtt atatccacaa tcccagcagc aagatgaagg gatgaaaaag gacacatgct      540
gccttccttt gaggagactt catctcactg gccaacactc agtcacatgt          590

```

<210> 47

<211> 774

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(774)

<223> n = A,T,C or G

<400> 47

```

acaagggggc ataatgaagg agtgggggana gatttttaaag aaggaaaaaa aacgaggccc      60
tgaacagaat tttcctgnac aacggggcct caaaataaatt ttcttgggga ggttcaagac      120
gcttcactgc ttgaaactta aatggatgtg ggacanaatt ttctgtaatg accctgaggg      180
cattacagac gggactctgg gaggaaggat aaacagaaaag gggacaaaagg ctaatcccaa      240
aacatcaaag aaaggaagggt ggcgtcatat ctcccagcct acacagttct ccagggtctt      300

```

```

cctcatccct ggaggacgac agtggaggaa caactgacca tgtccccagg ctctgtgtg 360
ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgtgat cctgcgtggc 420
ccacactcct tgaacacaca tccccagggt atattcctgg acatggctga acctcctatt 480
cctacttcg agatgccttg ctccctgcag cctgtcaaaa tccactcac cctccaaacc 540
acggcatggg aagcctttct gacttgctg attactccag catcttgga caatccctga 600
ttccccactc cttagaggca agataggggt gttaagagta gggctggacc acttgagacc 660
aggctgctgg cttcaaattn tggctcattt acgagctatg ggaccttggg caagtnatct 720
tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt 774

```

<210> 48

<211> 124

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(124)

<223> n = A,T,C or G

<400> 48

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canaaattga aattttataa aaaggcattt ttctcttata tccataaaat gatataattt 60
ttgcaantat anaaatgtgt cataaattat aatgttcctt aattacagct caacgcaact 120
tggt 124

```

<210> 49

<211> 147

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(147)

<223> n = A,T,C or G

<400> 49

```

gccgatgcta ctattttatt gcaggaggtg ggggtgtttt tattattctc tcaacagctt 60
tgtggctaca ggtgggtgtc gactgcatna aaaanttttt tacgggtgat tgcaaaaatt 120
ttagggcacc catatcccaa gcantgt 147

```

<210> 50

<211> 107

<212> DNA

<213> Homo sapien

<400> 50

```

acattaaatt aataaaagga ctgttggggt tctgctaaaa cacatggctt gatatatattgc 60
atggtttgag gttaggagga gttaggcata tgttttggga gaggggt 107

```

<210> 51

<211> 204

<212> DNA

<213> Homo sapien

<400> 51

```

gtcctaggaa gtctagggga cacacgactc tggggtcacg gggccgacac acttgacagg 60

```


cggaaggaa aggcagagaa gtgacaccgt cagggggaaa tgacagaaag gaaaatcaag	120
gccttgcaag gtcagaaagg ggactcaggg cttccaccac agccctgccc cacttgcca	180
cctccctttt gggaccagca atgt	204

<210> 52

<211> 491

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(491)

<223> n = A,T,C or G

<400> 52

acaaagataa catatatctt ataacaaaaa tttgatagtt ttaaagggtta gtattgtgta	60
gggtattttt caaaagacta aagagataac tcaggtaaaa agttagaaat gtataaaaca	120
ccatcagaca gggtttttaa aaacaacata ttacaaaatt agacaatcat ccttaaaaaa	180
aaaacttctt gtatcaatctt cttttgttca aaatgactga cttaantatt tttaaatatt	240
tcanaaacac ttcttcaaaa attttcaana tggtagcttt canatgtnc ctcagtccca	300
atgttgctca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctggggc	360
atgcaacagt gtcttttctt tnccttttct tttttttttt ttacaggcac agaaactcat	420
caattttatt tggataacaa agggctctcca aattatattg aaaaataaat ccaagttaat	480
atcactcttg t	491

<210> 53

<211> 484

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(484)

<223> n = A,T,C or G

<400> 53

acataattta gcagggctaa ttaccataag atgctattta ttaanaggtn tatgatctga	60
gtattaacag ttgctgaagt ttggattttt tatgcagcat tttctttttg ctttgataac	120
actacagaac ccttaaggac actgaaaatt agtaagtaaa gttcagaaac attagctgct	180
caatcaaadc tctacataac actatagtaa ttaaaacggt aaaaaaaagt gttgaaatct	240
gcactagtat anaccgctcc tgtcaggata anactgcttt ggaacagaaa gggaaaaanc	300
agctttgant ttctttgtgc tgatangagg aaaggctgaa ttaccttggt gcctctccct	360
aatgattggc aggtcnggta aatnccaaaa catattccaa ctcaacactt cttttccncc	420
tancctgant ctgtgtattc caggancagg cggtatggaat gggccagccc ncggatgttc	480
cant	484

<210> 54

<211> 151

<212> DNA

<213> Homo sapien

<400> 54

actaaacctc gtgcttgta actccatata gaaaacgggt ccatccctga acacggctgg	60
ccactgggta tactgctgac aaccgcaaca acaaaaaac aaatccttgg cactggctag	120
tctatgtcct ctcaagtgcc tttttgtttg t	151

<210> 55
<211> 91
<212> DNA
<213> Homo sapien

<400> 55
acctggcttg tctccgggtg gttcccggcg cccccacgg tccccagaac ggacactttc 60
gccctccagt ggatactcga gccaaagtgg t 91

<210> 56
<211> 133
<212> DNA
<213> Homo sapien

<400> 56
ggcggatgtg cgttgggttat atacaaatat gtcattttat gtaagggact tgagtatact 60
tggatttttg gtatctgtgg gttgggggga cgggtccagga accaatacc catggatacc 120
aagggacaac tgt 133

<210> 57
<211> 147
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(147)
<223> n = A,T,C or G

<400> 57
actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc 60
gactgggagc tgagcccttc cctttgcgcc tgcctcagag gattgttgcc gacntgcana 120
tctcantggg ctggatncat gcagggt 147

<210> 58
<211> 198
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(198)
<223> n = A,T,C or G

<400> 58
acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc 60
tgattacata catctatcct ttaaaaaaga tgtaaatctt aatttttatg ccacttatta 120
atttaccat gagttacctt gtaaatgaga agtcatgata gcactgaatt ttaactagtt 180
ttgacttcta agtttggg 198

<210> 59
<211> 330
<212> DNA
<213> Homo sapien

<400> 59

acaacaaatg ggttgtagg aagtcttacc agcaaaactg gtgatggcta ctgaaaagat	60
ccattgaaaa ttatcattaa tgattttaaa tgacaagtta tcaaaaactc actcaatttt	120
cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa	180
tacagtcaat aaatgacaaa gccagggcct acaggtgggt tccagacttt ccagacccag	240
cagaaggaat ctattttatc acatggatct ccgtctgtgc tcaaaatacc taatgatatt	300
tttcgtcttt attggacttc tttgaagagt	330

<210> 60

<211> 175

<212> DNA

<213> Homo sapien

<400> 60

accgtgggtg ccttctacat tcctgacggc tccttcacca acatctgggt ctacttcggc	60
gtcgtgggct ccttcctctt catcctcacc cagctgggtg tgctcatcga ctttgcgcac	120
tcctggaacc agcggtaggt gggcaaggcc gaggagtgcg attcccgtgc ctggt	175

<210> 61

<211> 154

<212> DNA

<213> Homo sapien

<400> 61

acccacttt tcctcctgtg agcagtctgg acttctcact gctacatgat gagggtagt	60
ggttggtgct cttcaacagt atcctccctt ttccggatct gctgagccgg acagcagtgc	120
tggactgcac agccccgggg ctccacattg ctgt	154

<210> 62

<211> 30

<212> DNA

<213> Homo sapien

<400> 62

cgctcgagcc ctatagtgag tcgtattaga	30
----------------------------------	----

<210> 63

<211> 89

<212> DNA

<213> Homo sapien

<400> 63

acaagtcatt tcagcaccct ttgctcttca aaactgacca tcttttatat ttaatgcttc	60
ctgtatgaat aaaaatggtt atgtcaagt	89

<210> 64

<211> 97

<212> DNA

<213> Homo sapien

<400> 64

accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag	60
aatcagtgc tccaggattg gtccttggat ctgggggt	97

<210> 65
 <211> 377
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (377)
 <223> n = A,T,C or G

<400> 65
 acaacaanaa ntcccttctt taggcactg atggaaacct ggaacccct tttgatggca 60
 gcatggcgctc ctaggccttg acacagcggc tggggtttgg gctntcccaa accgcacacc 120
 ccaacctgg tctaccacaca nttctggcta tgggctgtct ctgccactga acatcaggg 180
 tcggtcataa natgaaatcc caanggggac agaggtcagt agaggaagct caatgagaaa 240
 ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaacccg 300
 tgggggtgaa ctacccccan gaggaatcat gcctgggcga tgcaanggtg ccaacaggag 360
 gggcgggagg agcatgt 377

<210> 66
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 66
 acgcctttcc ctccagaattc agggaagaga ctgtcgctg ccttcctccg ttgttgctg 60
 agaaccctg tgcccttcc caccatatcc accctcgctc catctttgaa ctcaaacacg 120
 aggaactaac tgcacctgg tctctcccc agtccccagt tcacctcca tccctcacct 180
 tctccactc taagggatat caacactgcc cagcacagg gccctgaatt tatgtggtt 240
 ttatatattt tttataaaga tgcactttat gtcatttttt aataaagtct gaagaattac 300
 tgttt 305

<210> 67
 <211> 385
 <212> DNA
 <213> Homo sapien

<400> 67
 actacacaca ctccacttgc ctttgtgaga cactttgtcc cagcacttta ggaatgctga 60
 ggtcggacca gccacatctc atgtgcaaga ttgccagca gacatcaggt ctgagagttc 120
 cccttttaaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180
 tgtgctgtgc tggagattca cttttgagag agttctcctc tgagacctga tctttagagg 240
 ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgctg 300
 cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgcccatac 360
 catagtttct gtgctagtgg accgt 385

<210> 68
 <211> 73
 <212> DNA
 <213> Homo sapien

<400> 68
 acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60
 gtttttttaa tgg 73

<210> 69
 <211> 536
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(536)
 <223> n = A,T,C or G

<400> 69
 actagtccag tgtggtggaa ttccattgtg ttgggggctc tcaccctcct ctctgcagc 60
 tccagctttg tgcctgcct ctgaggagac catggcccag catctgagta ccctgctgct 120
 cctgctggcc accctagctg tggccctggc ctggagcccc aaggaggagg ataggataat 180
 cccgggtggc atctataacg cagacctcaa tgatgagtgg gtacagcgtg cccttcactt 240
 cgccatcagc gagtataaca aggccaccaa agatgactac tacagacgtc cgctgctgggt 300
 actaagagcc aggcaacaga ccgttggggg ggtgaattac ttcttcgacg tagaggtggg 360
 ccgaaccata tgtaccaagt ccagcccaa cttggacacc tgtgccttcc atgaacagcc 420
 agaactgcag aagaaacagt tgtgctcttt cgagatctac gaagtccct ggggagaaca 480
 gaangtcctt gggtgaaatc caggtgtcaa gaaatcctan ggatctgttg ccaggc 536

<210> 70
 <211> 477
 <212> DNA
 <213> Homo sapien

<400> 70
 atgacccta acaggggcc tctcagccct cctaagtacc tccggcctag ccattgtgatt 60
 tcacttccac tccataacgc tctctatact aggcctacta accaaccacac taaccatata 120
 ccaatgatgg cgcgatgtaa cagagaaaag cacataccaa ggccaccaca caccacctgt 180
 ccaaaaaggc cttcgatacg ggataatcct atttattacc tcagaagttt ttttcttcgc 240
 agggattttt ctgagccttt taccactcca gcctagcccc tacccccacaa ctaggaggggc 300
 actggccccc aacaggcatc accccgctaa atcccctaga agtccactc ctaaacacat 360
 ccgtattact cgcacagga gtatcaatca cctgagctca ccatagtcta atagaaaaca 420
 accgaaacca aattattcaa agcactgctt attacaattt tactgggtct ctatttt 477

<210> 71
 <211> 533
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(533)
 <223> n = A,T,C or G

<400> 71
 agagctatag gtacagtgtg atctcagctt tgcaaacaca ttttctacat agatagtact 60
 aggtattaat agatatgtaa agaaagaaat cacaccatta ataatggtaa gattgggttta 120
 tgtgattttt gtggtatttt tggcaccctt atatattgtt tccaaacttt cagcagtgat 180
 attattttca taacttaaaa agtgagtttg aaaaagaaaa tctccagcaa gcatctcatt 240
 taaataaagg tttgtcatct ttaaaaatac agcaatatgt gactttttta aaaagctgtc 300
 aaatagggtg gaccctacta ataattatta gaaatacatt taaaaacatc gagtacctca 360
 agtcagtttg ccttgaaaaa tatcaaatat aactcttaga gaaatgtaca taaaagaatg 420
 cttcgtaatt ttggagtang aggttcacct ctcaattttg tattttttaa aagtcacatg 480
 taaaaaaaaa aattcacaac agtatataag gctgtaaaat gaagaattct gcc 533

<210> 72
 <211> 511
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(511)
 <223> n = A,T,C or G

<400> 72
 tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcggtgta 60
 aaatgaaagg cttccaggca gttatctgat taaagaacac taaaagaggg acaaggctaa 120
 aagccgcagg atgtctacac tatancaggc gctatctggg ttggctggag gagctgtgga 180
 aaacatggan agattggtgc tgganacgc cgtggctatt cctcattgtt attacanagt 240
 gaggttctct gtgtgccac tggtttgaaa accgttctnc aataatgata gaatagtaca 300
 cacatgagaa ctgaaatggc ccaaaccag aaagaaagcc caactagatc ctcagaanac 360
 gcttctaggg acaataaccg atgaagaaaa gatggcctcc ttgtgcccc gtctgttatg 420
 atttctctcc attgcagcna naaacccgtt cttctaagca aacncagggt atgatggcna 480
 aaatacacc cctcttgaag naccnggagg a 511

<210> 73
 <211> 499
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(499)
 <223> n = A,T,C or G

<400> 73
 cagtgccagc actggtgcc a gtaccagtag caataacagt gccagtgcc gtgccagcac 60
 cagtggaggc ttcagtgtg gtgccagcct gaccgccact ctcacatttg ggctcttcgc 120
 tggccttggg ggagctggg ccagcaccag tggcagctct ggtgcctgtg gtttctccta 180
 caagttagat ttttagatatt gttaatcctg ccagtctttc tcttcaagcc aggggtgcac 240
 ctcagaaacc tactcaacac agcactctag gcagccacta tcaatcaatt gaagttgaca 300
 ctctgcatta aatctatttg ccatttctga aaaaaaaaa aaaaaaaggg cggccgctcg 360
 antctagagg gcccgtttaa acccgctgat cagcctcgac tgtgccttct anttgccagc 420
 catctgttgt ttgccctcc cccgntgcct tccttgacct tggaaagtgc cactcccact 480
 gtcctttcct aantaaat 499

<210> 74
 <211> 537
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(537)
 <223> n = A,T,C or G

<400> 74
 tttcatagga gaacacactg aggagatact tgaagaattt ggattcagcc gcgaagagat 60

```

ttatcagctt aactcagata aaatcattga aagtaataag gtaaaagcta gtctcctaact 120
tccaggccca cggctcaagt gaatttgaat actgcattta cagtgtagag taacacataa 180
cattgtatgc atggaaacat ggaggaacag tattacagtg tcttaccact ctaatcaaga 240
aaagaattac agactctgat tctacagtga tgattgaatt ctaaaaatgg taatcattag 300
ggcttttgat ttataanact ttgggtactt atactaaatt atggtagtta tactgccttc 360
cagtttgctt gatataattg ttgatattaa gattccttgac ttatattttg aatgggttct 420
actgaaaaan gaatgatata ttcttgaaga catcgatata catttattta cactcttgat 480
tctacaatgt agaaaatgaa ggaaatgccc caaattgtat ggtgataaaa gtcccggt 537

```

<210> 75

<211> 467

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(467)

<223> n = A,T,C or G

<400> 75

```

caaanacaat tgttcaaaag atgcaaatga tacactactg ctgcagctca caaacacctc 60
tgcatattac acgtacctcc tcctgctcct caagtagtgt ggtctatttt gccatcatca 120
cctgctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180
tggcacaagg aggccatctt ttctctcatcg gttattgtcc ctagaagcgt cttctgagga 240
tctagtggg ctttctttct ggggttgggc catctcantt ctcatgtgtg tactattcta 300
tcattattgt ataacggttt tcaaaccngt gggcacncag agaacctcac tctgtaataa 360
caatgaggaa tagccacggg gatctccagc accaaatctc tccatgttnt tccagagctc 420
ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tccctgn 467

```

<210> 76

<211> 400

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(400)

<223> n = A,T,C or G

<400> 76

```

aagctgacag cattcgggcc gagatgtctc gctccgtggc cttagctgtg ctgcgcgtac 60
tctctctttc tggcctggag gctatccagc gtactccaaa gattcagggt tactcacgtc 120
atccagcaga gaatggaaaag tcaaatttcc tgaattgcta tgtgtctggg ttcatccat 180
ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagt gagcattcag 240
acttgtcttt cagcaaggac tggcttttct atctcttgta ctacactgaa ttcaccccca 300
ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng 360
ttnagtggga tcganacatg taagcagcan catgggaggt 400

```

<210> 77

<211> 248

<212> DNA

<213> Homo sapien

<400> 77

```

ctggagtgcc ttgggtgtttc aagccctgc aggaagcaga atgcaccttc tgaggcacct 60

```

```

ccagctgccc cggcggggga tgcgaggctc ggagcaccct tgcccggctg tgattgctgc      120
caggcactgt tcatctcagc tttctgtcc ctttgctccc ggcaagcgct tctgctgaaa      180
gttcatatct ggagcctgat gtcttaacga ataaaggctc catgctccac ccgaaaaaaa      240
aaaaaaaaa                                     248

```

```

<210> 78
<211> 201
<212> DNA
<213> Homo sapien

```

```

<400> 78
actagtcag tgtggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca      60
tcaccagac cccgccctgc ccgtgcccc cgtgctgct aacgacagta tgatgcttac      120
tctgctactc ggaaactatt tttatgtaat taatgtatgc tttctgttt ataatgcct      180
gatttaaaaa aaaaaaaaaa a                                     201

```

```

<210> 79
<211> 552
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(552)
<223> n = A,T,C or G

```

```

<400> 79
tccttttgtt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg      60
tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt      120
cctctttcct ctgaagatta atgaagttga aaattgaggt ggataaatac aaaaaggtag      180
tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatataacc attcaaaatt      240
atgcaagtta gtaattactc agggttaact aaattacttt aatatgctgt tgaacctact      300
ctgttccttg gctagaaaaa attataaaca ggactttgtt agtttgggaa gccaaattga      360
taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tggaatttta      420
ttcccaggaa tatgggggtc atttatgaat antaccggg anagaagttt tgantnaaac      480
cngttttggt taatacgta atatgtcctn aatnaacaag gcntgactta tttccaaaaa      540
aaaaaaaaa aa                                     552

```

```

<210> 80
<211> 476
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(476)
<223> n = A,T,C or G

```

```

<400> 80
acagggattt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga      60
ggggaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca ccctggcct      120
cacacagact cccgagtagc tgggactaca ggcacacagt cactgaagca ggccctgttt      180
gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtacta      240
aggttaaact ttcccacca gaaaaggcaa cttagataaa atcttagagt actttcatac      300
tcttctaagt cctcttcag cctcactttg agtcctcctt gggggttgat aggaantntc      360

```



```

tcttggtttt ctcaataaaa tctctatcca tctcatgttt aatttggtac gcntaaaaat      420
gctgaaaaaa ttaaaatgtt ctggtttcnc tttaaaaaaa aaaaaaaaaa aaaaaa      476

```

```

<210> 81
<211> 232
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(232)
<223> n = A,T,C or G

```

```

<400> 81
tttttttttg tatgcntcn ctgtgnggtt attgttgctg ccacctgga ggagccagct      60
ttcttctgta tctttctttt ctgggggata ttcttggtct tggccctcca tccccagcct      120
ctcatcccca tcttgcaatt ttgctagggg tggaggcgct ttcttggtag cccctcagag      180
actcagtcag cggaataag tcctaggggt ggggggtgtg gcaagccggc ct      232

```

```

<210> 82
<211> 383
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

```

```

<400> 82
aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc      60
agtaccagta ccaataacat gccagtgccg gtgccagcac cagtgggtggc ttcagtgtct      120
gtgccagcct gaccgccact ctcacatttg ggctcttcgc tggccttggg ggagctgggt      180
ccagcaccag tggcagctct ggtgcctgtg gtttctccta caagtgagat tttagatatt      240
gttaatcctg ccagtctttc tcttcaagcc aggggtgcac ctcagaaacc tactcaacac      300
agcactctng gcagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg      360
ccatttcaaa aaaaaaaaaa aaa      383

```

```

<210> 83
<211> 494
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(494)
<223> n = A,T,C or G

```

```

<400> 83
accgaattgg gaccgctggc ttataagcga tcatgtcctc cagtattacc tcaacgagca      60
gggagatcga gtctatacgc tgaagaaatt tgaccgatg ggacaacaga cctgtctcagc      120
ccatcctgct cggttctccc cagatgacaa atactctcga caccgaatca ccatcaagaa      180
acgcttcaag gtgctcatga cccagcaacc gcgcctgtc ctctgagggt ccttaaactg      240
atgtcttttc tgccacctgt taccctcgg agactccgta accaaactct tcggactgtg      300
agccctgatg cctttttgcc agccatactc tttggcntcc agtctctcgt ggcgattgat      360

```

```

tatgcttggtg tgaggcaatc atggtggcat caccatnaa gggaacacat ttganttttt 420
tttcncatat tttaaattac naccagaata nttcagaata aatgaattga aaaactctta 480
aaaaaaaaaa aaaa 494

```

<210> 84

<211> 380

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(380)

<223> n = A,T,C or G

<400> 84

```

gctggtagcc tatggcgtgg ccacggangg gctcctgagg cacgggacag tgacttccca 60
agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag 120
gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttctgg 180
gcacacccctc ctggggccca ggcgggcacc tgcgtctccc agtatgcaa ctggctgggtg 240
gtgctgctcc tcgtcatctt cctgctcgtg gccaacatcc tgctggtcac ttgctcattg 300
ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc 360
agcgttnccg cctcatccgg 380

```

<210> 85

<211> 481

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(481)

<223> n = A,T,C or G

<400> 85

```

gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggctctctgc ttcataccgc 60
tnccatcgtc atactgtagg tttgccacca cctcctgcat cttggggcgg ctaatatcca 120
ggaaactctc aatcaagtca ccgtcnatna aacctgtggc tggttctgtc ttccgctcgg 180
tgtgaaagga tctccagaag gagtgctcga tcttccccac acttttgatg actttattga 240
gtcgattctg catgtccagc aggaggttgt accagctctc tgacagtgag gtcaccagcc 300
ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgtggggggg gnagtctcac 360
ccagattctg cattaccaga nagccgtggc aaaaganatt gacaactcgc ccaggngaa 420
aaagaacacc tcttgggaagt gctngccgct cctcgtccnt tggtggnngc gcntnccttt 480
t 481

```

<210> 86

<211> 472

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(472)

<223> n = A,T,C or G

<400> 86

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aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt      60
acttggaata gcaacttnaa gcctggacac tggattataa attcacaata tgcaacactt      120
taaacagtgt gtcaatctgc tcccttactt tgtcatcacc agtctgggaa taagggtatg      180
ccctattcac acctgttaaa agggcgctaa gcatttttga ttcaacatct ttttttttga      240
cacaagtccg aaaaaagcaa aagtaaagcag ttnttaattt gttagccaat tcactttctt      300
catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg      360
atatntgagc ggaagantag cctttctact tcaccagaca caactccttt catattggga      420
tgttnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg              472
```

<210> 87

<211> 413

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(413)

<223> n = A,T,C or G

<400> 87

```
agaaaccagt atctctnaaa acaacctctc ataccttgtg gacctaatTT tgtgtgctg      60
tgtgtgtgcg cgcattatat atagacaggc acatcttttt tacttttgta aaagcttatg      120
cctcttttgt atctatatct gtgaaagtTT taatgatctg ccataatgtc ttggggacct      180
ttgtcttctg tgtaaagtgt actagagaaa acacctatnt tatgagtcaa tctagttngt      240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc cttgactagg      300
ggggacaaag aaaagcnaaa ctgaacatna gaaacaattn cctggtgaga aattncataa      360
acagaaattg ggtngtatat tgaaanannn catcattnaa acgttttttt ttt              413
```

<210> 88

<211> 448

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(448)

<223> n = A,T,C or G

<400> 88

```
cgcagcgggt cctctctatc tagctccagc ctctcgctg cccactccc cgcgtcccgc      60
gtcctagccn accatggccg ggcccctgcg cgcccctgctg ctctgctgg ccactctggc      120
cgtggccctg gccgtgagcc ccgcggcccg ctccagtcct ggcaagccgc cgcgcctggt      180
gggaggccca tggaccccg gtggaagaag aagggtgtg cggtgcactg gactttgccg      240
tcggcnanta caacaaaccc gcaacnactt ttaccnagcn cgcgtgcag gttgtgccgc      300
cccaancaa ttgttactng gggttaantaa ttcttggaag ttgaacctgg gccaaacnng      360
tttaccagaa ccnagccaat tngaacaatt ncccctccat aacagcccct tttaaaaagg      420
gaancantcc tgntcttttc caaatTTT              448
```

<210> 89

<211> 463

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(463)

<223> n = A,T,C or G

<400> 89

```
gaattttgtg cactggccac tgtgatggaa ccattggggc aggatgcttt gagtttatca    60
gtagtgattc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaattagc    120
agaggcttag gtctgcatat cagcagacag tttgtccgtg tattttttag ccttgaagtt    180
ctcagtgaca agttnnttct gatgcgaagt tctnatccca gtgttttagt cctttgcatc    240
tttnatgtnn agacttgcct ctntnaaatt gcttttgnnt tctgcaggta ctatctgtgg    300
tttaacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn    360
aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn    420
aattcnnana anttcagntn tcatacaaca naacngganc ccc                        463
```

<210> 90

<211> 400

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(400)

<223> n = A,T,C or G

<400> 90

```
agggattgaa ggtctnttnt actgtcggac tgttcancca ccaactctac aagttgctgt    60
cttcactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaaciaat    120
tcttcaccag tcacatcttc taggaccttt ttggattcag ttagtataag ctcttcact    180
tcctttgtta agacttcac tcggtaaagtc ttaagttttg tagaaaggaa ttaattgct    240
cgttctctaa caatgtcctc tccttgaagt atttggtga acaaccacc tnaagtcct    300
ttgtgcatcc attttaaata tacttaatat ggcattggtt cactagggtt aattctgcaa    360
gagtcactctg tctgcaaaag ttgcgttagt atatctycca                        400
```

<210> 91

<211> 480

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(480)

<223> n = A,T,C or G

<400> 91

```
gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact    60
ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac    120
atgcctcttt gactaccgtg tgccagtgtt ggtgattctc acacacctcc nncgcctctt    180
tgtggaaaaa ctggcacttg nctggaaacta gcaagacatc acttacaaat tcaccacga    240
gacacttgaa aggtgtaaca aagcgactct tgcattgctt tttgtccctc cggcaccagt    300
tgtcaatact aaccgcgtgg tttgcctcca tcacatttgt gatctgtagc tctggataca    360
tctcctgaca gtactgaaga acttcttctt ttgtttcaaa agcaactctt ggtgcctggt    420
ngatcaggtt cccatttccc agtcggaatg ttcacatggc atatnttact tcccacaaaa    480
```

<210> 92

<211> 477

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(477)

<223> n = A,T,C or G

<400> 92

atacagccca	natcccacca	cgaagatgcg	cttggtgact	gagaacctga	tgcggtcact	60
ggccccgctg	tagccccagc	gactctccac	ctgctggaag	cggttgatgc	tgcactcctt	120
cccacgcagg	cagcagcggg	gccggccaat	gaactccact	cgtggcttgg	ggttgacggg	180
taantgcagg	aagaggctga	ccacctcgcg	gtccaccagg	atgcccgaact	gtgcgggacc	240
tgcagcgaaa	ctcctcgatg	gtcatgagcg	ggaagcgaat	gangcccagg	gccttgccca	300
gaaccttccg	cctgttctct	ggcgtcacct	gcagctgctg	ccgctnacac	tcggcctcgg	360
accagcggac	aaacggcggt	gaacagccgc	acctcacgga	tgcccantgt	gtcgcgctcc	420
aggaacggcn	ccagcgtgtc	caggtcaatg	tcggtgaanc	ctccgcgggt	aatggcg	477

<210> 93

<211> 377

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(377)

<223> n = A,T,C or G

<400> 93

gaacggctgg	accttgccctc	gcattgtgct	gctggcagga	ataccttggc	aagcagctcc	60
agtccgagca	gccccagacc	gctgccgccc	gaagctaagc	ctgcctctgg	ccttccccctc	120
cgcttcaatg	cagaaccant	agtgggagca	ctgtgtttag	agttaagagt	gaacactgtn	180
tgattttact	tggaatttc	ctctgtttata	tagcttttcc	caatgctaata	ttccaaacaa	240
caacaacaaa	ataacatggt	tgctgtttna	gttgataaaa	agtangtgat	tctgtatnta	300
aagaaaatat	tactgtttaca	tatactgctt	gcaantttctg	tatttattgg	tnctctggaa	360
ataaatatat	tattaaa					377

<210> 94

<211> 495

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(495)

<223> n = A,T,C or G

<400> 94

ccctttgagg	ggttagggtc	cagttcccag	tggaagaaac	aggccaggag	aantgcgtgc	60
cgagctgang	cagatttccc	acagtgaccc	cagagccctg	ggctatagtc	tctgaccctt	120
ccaaggaaag	accaccttct	ggggacatgg	gctggagggc	aggacctaga	ggcaccaagg	180
gaaggcccca	ttccggggct	gttccccgag	gaggaaggga	aggggctctg	tgtgcccccc	240
acgaggaana	ggccctgant	cctgggatca	nacacccctt	cacgtgtatc	cccacacaaa	300
tgcaagctca	ccaaggtccc	ctctcagtc	cttccctaca	ccctgaacgg	ncaactggccc	360
acaccacccc	agancancca	cccgcctatg	ggaatgtntc	caaggaatcg	cngggcaacg	420
tggactctng	ttccnnaagg	gggcagaatc	tccaatagan	gganngaacc	cttgctnana	480

aaaaaaaaana aaaaaa

495

<210> 95

<211> 472

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(472)

<223> n = A,T,C or G

<400> 95

ggttacttgg	tttcattgcc	accacttagt	ggatgtcatt	tagaaccatt	ttgtctgctc	60
cctctggaag	ccttgcgcag	agcggacttt	gtaattgttg	gagaataact	gctgaatttt	120
tagctgtttt	gagttgattc	gcaccactgc	accacaactc	aatatgaaaa	ctatttnact	180
tatttattat	cttgtgaaaa	gtatacaatg	aaaattttgt	tcatactgta	tttatcaagt	240
atgatgaaaa	gcaatagata	tatattcttt	tattatgttn	aattatgatt	gccattatta	300
atcggaacaa	tgtggagtgt	atgttctttt	cacagtaata	tatgcctttt	gtaacttcac	360
ttggttattt	tattgtaaat	gaattacaaa	attcttaatt	taagaaaatg	gtangttata	420
tttanttcan	taatttcttt	ccttgtttac	gttaattttg	aaaagaatgc	at	472

<210> 96

<211> 476

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(476)

<223> n = A,T,C or G

<400> 96

ctgaagcatt	tcttcaaact	tntctacttt	tgtcattgat	acctgtagta	agttgacaat	60
gtggtgaaat	ttcaaaatta	tatgtaactt	ctactagttt	tactttctcc	cccaagtctt	120
ttttaactca	tgatttttac	acacacaatc	cagaacttat	tatatagcct	ctaagtcttt	180
attcttcaca	gtagatgatg	aaagagtcct	ccagtgtctt	gngcanaatg	ttctagntat	240
agctggatac	atacngtggg	agttctataa	actcatacct	cagtgggact	naacccaaat	300
tgtgttagtc	tcaattccta	ccacactgag	ggagcctccc	aaatcactat	attcttatct	360
gcaggtactc	ctccagaaaa	acngacaggg	caggcttgca	tgaaaaagtn	acatctgcgt	420
tacaaaagtct	atcttcctca	nangtctgtn	aaggaacaat	ttaatcttct	agcttt	476

<210> 97

<211> 479

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(479)

<223> n = A,T,C or G

<400> 97

actcttttcta	atgctgatata	gatcttgagt	ataagaatgc	atatgtcact	agaatggata	60
aaataatgct	gcaaacttaa	tgttcttatg	caaatggaa	cgctaatgaa	acacagctta	120

caatcgcaaa tcaaaactca caagtgtctca tctgtttag atttagtgtg ataagactta	180
gattgtgctc cttcggatat gattgtttct canatcttgg gcaatnttcc ttagtcaaat	240
caggctacta gaattctgtt attggatatn tgagagcatg aaatttttaa naatacactt	300
gtgattatna aattaatcac aaatttcact tatacctgct atcagcagct agaaaaacat	360
ntnnttttta natcaaagta ttttgtgttt ggaantgtnn aaatgaaatc tgaatgtggg	420
ttcnatctta ttttttcccn gacnactant tnccttttta gggncatttc tganccatc	479

<210> 98

<211> 461

<212> DNA

<213> Homo sapien

<400> 98

agtgacttgt cctccaacaa aacccttga tcaagttgt ggcactgaca atcagaccta	60
tgctagtcc tgctatctat tcgctactaa atgcagactg gaggggacca aaaaggggca	120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga	180
agtgattcag tttcctctac ggatgagaga ctggctcaag aatatactca tgcagcttta	240
tgaagccact ctgaacacgc tggttatcta gatgagaaca gagaaataaa gtcagaaaat	300
ttacctggag aaaagaggct ttggctgggg accatcccat tgaaccttct cttaggact	360
ttaagaaaaa ctaccacatg ttgtgtatcc tggcgccggc cgtttatgaa ctgaccaccc	420
tttggaataa tcttgacgct cctgaacttg ctccctctgcg a	461

<210> 99

<211> 171

<212> DNA

<213> Homo sapien

<400> 99

gtggcgcgc gcaggtgttt cctcgtaccg cagggccccc tcccttcccc aggcgtccct	60
cggcgccctc gcgggcccga ggaggagcgg ctggcgggtg gggggagtgt gacccacct	120
cggtgagaaa agccttctct agcgatctga gaggcgtgcc ttgggggtac c	171

<210> 100

<211> 269

<212> DNA

<213> Homo sapien

<400> 100

cggccgcaag tgcaactcca gctggggccg tgcggacgaa gattctgccg gcagttggtc	60
cgactgcgac gacggcggcg gcgacagtcg caggtgcagc gcgggcgcct ggggtcttgc	120
aaggctgagc tgacgccgca gaggtcgtgt cacgtcccac gaccttgacg ccgtcgggga	180
cagccggaac agagcccgtt gaagcgggag gcctcgggga gcccctcggg aaggcgggc	240
cgagagatac gcaggtgcag gtggccgcg	269

<210> 101

<211> 405

<212> DNA

<213> Homo sapien

<400> 101

ttttttttt ttttgaatc tactgcgagc acagcaggtc agcaacaagt ttattttgca	60
gctagcaagg taacagggtg gggcatggtt acatgttcag gtcaacttcc ttgtcgtgg	120
ttgattggtt tgtctttatg ggggcggggt ggggtagggg aaacgaagca aataacatgg	180
agtgggtgca cctccctgt agaacctggt taaaaagctt ggggcagttc acctggctg	240
tgaccgtcat tttcttgaca tcaatgttat tagaagtcag gatattcttt agagagtcca	300

```

ctgtttctgga gggagattag ggtttcttgc caaatccaac aaaatccact gaaaaagttg      360
gatgatcagt acgaataccg aggcataattc tcatatcggg ggcca                        405

```

```

<210> 102
<211> 470
<212> DNA
<213> Homo sapien

```

```

<400> 102
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt      60
ggcacttaat ccatttttat ttcaaaatgt ctacaaattt aatcccattha tacgggtattt      120
tcaaaatcta aattattcaa attagccaaa tccttaccaa ataataccca aaaatcaaaa      180
atatacttct ttcagcaaac ttgttacata aattaaataa atatatacgg ctgggtgtttt      240
caaagtacaa ttatcttaac actgcaaaaca ttttaaggaa ctaaaataaa aaaaaacact      300
ccgcaaagggt taaagggaac aacaaattct tttacaacac cattataaaa atcatatctc      360
aaatcttagg ggaatatata cttcacacgg gatcttaact ttacttact ttgtttattt      420
ttttaaacca ttgtttgggc ccaacacaat ggaatccccc ctggactagt                    470

```

```

<210> 103
<211> 581
<212> DNA
<213> Homo sapien

```

```

<400> 103
tttttttttt ttttttttga cccccctctt ataaaaaaca agttaccatt ttatttttact      60
tacacatatt tattttataa ttggtattag atattcaaaa ggcagctttt aaaatcaaac      120
taaatggaaa ctgccttaga tacataattc ttagggaatta gcttaaaatc tgcctaaagt      180
gaaaatcttc tctagctctt ttgactgtaa atttttgact cttgtaaaac atccaaattc      240
atttttcttg tctttaaaat tatctaattc ttccattttt tccctattcc aagtcaattt      300
gcttctctag cctcatttcc tagctcttat ctactattag taagtggctt ttttccataa      360
agggaaaaca ggaagagaaa tggcacacaa aacaaacatt ttatattcat atttctacct      420
acgttaataa aatagcattt tgtgaagcca gctcaaaaga aggcttagat ccttttatgt      480
ccatttttagt cactaaacga tatcaaagtg ccagaatgca aaagggtttgt gaacatttat      540
tcaaaagcta atataagata tttcacatac tcatctttct g                                581

```

```

<210> 104
<211> 578
<212> DNA
<213> Homo sapien

```

```

<400> 104
tttttttttt tttttttttt tttttctctt cttttttttt gaaatgagga tgcagttttt      60
cactctctag atagggcatg aagaaaactc atctttccag ctttaaaata acaatcaaat      120
ctcttatgct atatcatatt ttaagttaaa ctaatgagtc actggcttat cttctcctga      180
aggaaatctg ttcattcttc tcattcatat agttatatca agtactacct tgcataattga      240
gagggtttttc ttctctattt acacatatat ttccatgtga atttgtatca aacctttatt      300
ttcatgcaa ctagaaaata atgtttcttt tgcataagag aagagaacaa tatagcatta      360
caaaactgct caaattgttt gttaagttaa ccattataat tagttggcag gagctaatac      420
aatcacatt tacgacagca ataataaaac tgaagtacca gttaaatatc caaaataatt      480
aaaggaacat ttttagcctg ggtataatta gctaattcac tttacaagca tttattagaa      540
tgaattcaca tgttattatt cctagcccaa cacaatgg                                578

```

```

<210> 105
<211> 538
<212> DNA

```


<213> Homo sapien

<400> 105

tttttttttt	tttttcagta	ataatcagaa	caatatttat	ttttatattt	aaaattcata	60
gaaaagtgcc	ttacatttaa	taaaagtttg	tttctcaaag	tgatcagagg	aattagatat	120
gtcttgaaca	ccaatattaa	tttgaggaaa	atacaccaaa	atacattaag	taaattattt	180
aagatcatag	agcttgtaag	tgaaaagata	aaatttgacc	tcagaaactc	tgagcattaa	240
aaatccacta	ttagcaaata	aattactatg	gacttccttg	tttaattttg	tgatgaatat	300
ggggtgtcac	tggtaaacca	acacattctg	aaggatacat	tacttagtga	tagattctta	360
tgtactttgc	taatacgtgg	atatgagttg	acaagtttct	ctttcttcaa	tcttttaagg	420
ggcgagaaat	gaggaagaaa	agaaaaggat	tacgcatact	gttctttcta	tggaaggatt	480
agatatgttt	cctttgccaa	tattaaaaaa	ataataatgt	ttactactag	tgaaaccc	538

<210> 106

<211> 473

<212> DNA

<213> Homo sapien

<400> 106

tttttttttt	tttttttagtc	aagttttctat	ttttattata	attaaagtct	cggtcatttc	60
atttattagc	tctgcaactt	acatatttaa	attaaagaaa	cgtttttagac	aactgtacaa	120
tttataaatg	taagggtgcc	ttattgagta	atatattcct	ccaagagtgg	atgtgtccct	180
tctccacca	actaatgaac	agcaacatta	gtttaatttt	attagtagat	atacactgct	240
gcaaacgcta	attctcttct	ccatcccat	gtgatattgt	gtatatgtgt	gagttggtag	300
aatgcatcac	aatctacaat	caacagcaag	atgaagctag	gctgggcttt	cggtgaaaat	360
agactgtgtc	tgtctgaatc	aaatgatctg	acctatcctc	ggtggcaaga	actcttcgaa	420
ccgcttctc	aaaggcgctg	ccacatttgt	ggctctttgc	acttgtttca	aaa	473

<210> 107

<211> 1621

<212> DNA

<213> Homo sapien

<400> 107

cgccatggca	ctgcagggca	tctcggtcat	ggagctgtcc	ggcctggccc	cgggcccgtt	60
ctgtgctatg	gtcctggctg	acttcggggc	gcgtgtggta	cgcgtggacc	ggcccggctc	120
ccgctacgac	gtgagccgct	tgggcccggg	caagcgctcg	ctagtgtggt	acctgaagca	180
gccgcgggga	gccgcggtgc	tgcggcgctc	gtgcaagcgg	tcggatgtgc	tgctggagcc	240
cttcgccgcg	ggtgtcatgg	agaaactcca	gctgggccc	gagattctgc	agcgggaaaa	300
tccaaggctt	atttatgcca	ggctgagttg	atttgccag	tcaggaagct	tctgccggtt	360
agctggccac	gatatcaact	atttggttt	gtcaggtgtt	ctctcaaaaa	ttggcagaag	420
tggtgagaat	ccgtatgccc	cgctgaatct	cctggctgac	tttgctggtg	gtggccttat	480
gtgtgcactg	ggcattataa	tggctctttt	tgaccgcaca	cgcactgaca	agggtcaggt	540
cattgatgca	aatatggtgg	aaggaacagc	atatttaagt	tcttttctgt	ggaaaactca	600
gaaatcgagt	ctgtgggaag	cacctcgagg	acagaacatg	ttggatgggt	gagcaccttt	660
ctatacgact	tacaggacag	cagatgggga	attcatggct	gttgagacaa	tagaacccca	720
gttctacgag	ctgctgatca	aaggacttgg	actaaagtct	gatgaacttc	ccaatcagat	780
gagcatggat	gattggccag	aaatgaagaa	gaagtttgca	gatgtatttg	caaagaagac	840
gaaggcagag	tggtgtcaaa	tctttgacgg	cacagatgcc	tgtgtgactc	cggttctgac	900
ttttgaggag	gttgttcata	atgatcacia	caaggaacgg	ggctcgttta	tcaccagtga	960
ggagcaggac	gtgagccccc	gccctgcacc	tctgtgttta	aacaccccag	ccatcccttc	1020
tttcaaaaag	gataccttca	taggagaaca	cactgaggag	atacttgaag	aatttggatt	1080
cagccgcgaa	gagattttatc	agcttaactc	agataaaatc	attgaaagta	ataaggtaaa	1140
agctagtctc	taacttccag	gccacggct	caagtgaatt	tgaatactgc	atttacagtg	1200
tagagtaaca	cataacattg	tatgcatgga	aacatggagg	aacagtatta	cagtgtccta	1260

```

ccactctaatt caagaaaaga attacagact ctgattctac agtgaatgatt gaattctaaa 1320
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atttacactc ttgattctac aatgtagaaa atgaggaaat gccacaaatt gtatgggtgat 1560
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a 1621

```

```

<210> 108
<211> 382
<212> PRT
<213> Homo sapien

```

```

<400> 108
Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1      5      10      15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20     25     30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35     40     45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50     55     60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65     70     75     80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85     90     95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100    105    110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115    120    125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130    135    140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145    150    155    160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165    170    175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180    185    190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195    200    205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
210    215    220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225    230    235    240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
245    250    255
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
260    265    270
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
275    280    285
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
290    295    300
His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
305    310    315    320
Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala

```

```
<210> 109
<211> 1524
<212> DNA
<213> Homo sapien
```

```
<210> 110
<211> 3410
<212> DNA
<213> Homo sapien
```

<400> 110						
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aagctggacc	ggcaccaaag	ggctggcaga	aatgggcgcc	tggctgattc	ctaggcagtt	180
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gagtgcctga	acggccccct	gagccctacc	cgcttgcccc	actatggtcc	agaggctgtg	300
ggtgagccgc	ctgctgcggc	accggaagac	ccagctcttg	ctggtcaacc	tgctaacctt	360
tggcctggag	gtgtgtttgg	ccgcaggcat	cacctatgtg	ccgctctcgc	tgctggaagt	420
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ctgtgtcccg	ctcctaggct	cagccagtga	ccactggcgt	ggacgctatg	gccgccgccg	540
gcccttcac	tgggcactgt	ccttgggcat	cctgctgagc	ctctttctca	tcccaagggc	600
cggctggcta	gcagggtgc	tgtgcccga	tcccaggcc	ctggagctgg	cactgctcat	660
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catgatcagt	cttggggggt	gcctgggcta	cctcctgcct	gccattgact	gggacaccag	840
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gcaggaccag	aagcacaag	tgcggtttcc	caagcctttg	tccatctcag	ccccagagt	3120
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gaggtcttat	ctctcagggg	gggtttaagt	gccgtttgca	ataatgtcgt	cttattttatt	3240
tagcgggggt	aatattttat	actgtaagt	agcaatcaga	gtataatgtt	tatggtgaca	3300
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aaaaaaaaara	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		3410

<210> 111

<211> 1289

<212> DNA

<213> Homo sapien

<400> 111

```

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ccatgcagtg cttcagcttc attaagacca tgatgatcct cttcaatttg ctcactcttc      180
tgtgtggtgc agccctgttg gcagtgggca tctgggtgtc aatcgatggg gcactccttc      240
tgaagatctt cgggccactg tcgtccagtg ccatgcagt tgtcaacgtg ggctacttcc      300
tcacgcagc cggcggtgtg gtctttgtct ttggtttcct gggctgctat ggtgctaaga      360
ctgagagcaa gtgtgccctc gtgacgttct tcttcactct cctcctcatc ttcattgctg      420
agggtgcagc tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttcctgacgt      480
tgctggtagt gcctgccatc aagaaagatt atggttccca ggaagacttc actcaagtgt      540
ggaacaccac catgaaaggg ctcaagtgtc gtggcttcac caactatacg gattttgagg      600
actcacccta cttcaaagag aacagtgcct tcccccatc ctggtgcaat gacaacgtca      660
ccaacacagc caatgaaacc tgcaccaagc aaaaggctca cgacacaaaa gttaggggtt      720
gcttcaatca gcttttgtat gacatccgaa ctatgcagt caccgtgggt ggtgtggcag      780
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tacaataagt ccacttctgc ctctgccact actgtgcca catgggaact gtgaagaggc      900
accctggcaa gcagcagtga ttgggggagg ggacaggatc taacaatgtc acttgggcca      960
gaatggacct gccctttctg ctccagactt ggggctagat agggaccact ccttttagcg     1020
atgcctgact ttccttccat tgggtgggtg atgggtgggg ggcattccag agcctctaag     1080
gtagccagtt ctgttgcccc tccccccagt ctattaaacc cttgatatgc cccctaggcc     1140
tagtggtgat cccagtgtc tactggggga tgagagaaag gcattttata gcctgggcat     1200
aagtgaatc agcagagcct ctgggtggat gtgtagaagg cacttcaaaa tgcataaacc     1260
tgttacaatg ttaaaaaaaaa aaaaaaaaaa                                     1289

```

<210> 112

<211> 315

<212> PRT

<213> Homo sapien

<400> 112

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
 1              5              10              15
Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
      20              25              30
Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
      35              40              45
Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
      50              55              60
Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
      65              70              75              80
Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
      85              90              95
Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
      100             105             110
Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
      115             120             125
Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
      130             135             140
Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
      145             150             155             160
Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
      165             170             175
Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
      180             185             190
Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu

```

```

      195                200                205
His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
  210                215                220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
  225                230                235                240
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
      245                250                255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
      260                265                270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
      275                280                285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
      290                295                300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
  305                310                315

```

<210> 113

<211> 553

<212> PRT

<213> Homo sapien

<400> 113

```

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
  1                5                10                15
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
      20                25                30
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
      35                40                45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
      50                55                60
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
      65                70                75                80
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
      85                90                95
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
      100                105                110
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
      115                120                125
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
      130                135                140
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
      145                150                155                160
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
      165                170                175
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
      180                185                190
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
      195                200                205
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
      210                215                220
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
      225                230                235                240
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
      245                250                255
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg

```

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      260      265      270
Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
      275      280      285
Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
      290      295      300
Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
      305      310      315      320
Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
      325      330      335
Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
      340      345      350
Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
      355      360      365
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
      370      375      380
Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
      385      390      395      400
Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
      405      410      415
Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
      420      425      430
Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
      435      440      445
Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
      450      455      460
Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
      465      470      475      480
Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
      485      490      495
Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
      500      505      510
Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
      515      520      525
Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
      530      535      540
Lys Ser Asp Leu Ala Lys Tyr Ser Ala
      545      550

```

<210> 114

<211> 241

<212> PRT

<213> Homo sapien

<400> 114

```

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
1      5      10      15
Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
20      25      30
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
35      40      45
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
50      55      60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
65      70      75      80
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile

```

[illegible]

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<210> 115
<211> 366
<212> DNA
<213> Homo sapien
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<400> 115							
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catttcactg	tgatgtatat	tgtgttgcaa	aaaaaaaaa	gtgtctttgt	ttaaaattac		120
ttggttttg	aatccatctt	gctttttccc	cattggaact	agtcattaac	ccatctctga		180
actggtagaa	aaacatctga	agagctagtc	tatcagcatc	tgacagggtg	attggatggg		240
tctcagaacc	atttcaccca	gacagcctgt	ttctatcctg	tttaataaat	tagtttgggt		300
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ttagtc							366

```
<210> 116
<211> 282
<212> DNA
<213> Homo sapien
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<220>  
<221> misc_feature  
<222> (1)...(282)  
<223> n = A,T,C or G
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<400>	116								
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gagaaatgag	atnaaacaca	atnttataaa	gtctacttag	agaagatcaa	gtgacctcaa				120
agacttttact	attttcatat	tttaagacac	atgattttatc	ctattttagt	aacctgggttc				180
atacgtttaaa	caaaggataa	tgtgaacagc	agagaggatt	tgttggcaga	aaatctatgt				240
tcaatctnga	actatctana	tcgacagacat	ttctattcct	tt					282

<210> 117
<211> 305

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(305)

<223> n = A,T,C or G

<400> 117

acacatgtcg cttcactgcc ttcttagatg cttctgggtca acatanagga acagggacca	60
tatttatacct ccttcctgaa acaattgcaa aataanaaaa aatatatgaa acaattgcaa	120
aataaggcaa aatatatgaa acaacagggtc tcgagatatt ggaaatcagt caatgaagga	180
tactgatccc tgatcactgt cctaatagcag gatgtgggaa acagatgagg tcacctctgt	240
gactgcccc gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat	300
tggt	305

<210> 118

<211> 71

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(71)

<223> n = A,T,C or G

<400> 118

accaaggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa	60
aantcctggg t	71

<210> 119

<211> 212

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(212)

<223> n = A,T,C or G

<400> 119

actccggttg gtgtcagcag cacgtggcat tgaacatngc aatgtggagc ccaaaccaca	60
gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac	120
agtaagctgg cccttctaataaaaagaaaat tgaaaggttt ctactaanc ggaattaant	180
aatggantca aganactccc aggcctcagc gt	212

<210> 120

<211> 90

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(90)

<223> n = A,T,C or G

```

<400> 120
actcgttgca natcaggggc cccccagagt caccgttgca ggagtccttc tggctcttgcc 60
ctccgccggc gcagaacatg ctgggggtggt 90

<210> 121
<211> 218
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(218)
<223> n = A,T,C or G

<400> 121
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gaataagatt tgctaaaaga tttggggcta aaacatgggtt attgggagac atttctgaag 120
atatncangt aaattangga atgaattcat gggtcttttg ggaattcctt tacgatngcc 180
agcatanact tcatgtgggg atancagcta cccttgta 218

<210> 122
<211> 171
<212> DNA
<213> Homo sapien

<400> 122
taggggtgta tgcaactgta aggacaaaaa ttgagactca actggcttaa ccaataaagg 60
catttgtag ctcatggaac aggaagtcgg atgggtggggc atcttcagtg ctgcatgagt 120
caccaccccg gcgggggtcat ctgtgccaca ggtccctgtt gacagtgcgg t 171

<210> 123
<211> 76
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(76)
<223> n = A,T,C or G

<400> 123
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ttatcaanta ttgtgt 76

<210> 124
<211> 131
<212> DNA
<213> Homo sapien

<400> 124
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caatgtgctg ggtcatatgg aggggaggag actctaaaat agccaatttt attctcttgg 120
ttaagatttg t 131

```

<210> 125
 <211> 432
 <212> DNA
 <213> Homo sapien

<400> 125
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 cttgaaaaag aggtgatagc tcttcagagg acttggtgact tttgctcaga tgctgaagaa 120
 ctacagtctg catttggcag aaatgaagat gaatttggat taaatgagga tgctgaagat 180
 ttgcctcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg 240
 ctcttgaggt atcagtcact tttgagaatg tttcttagtt actgcatact tcatggatcc 300
 catggtgggg gtcttgcacg tgtaagaatg gaattgattt tgcttttgca agaattctcag 360
 caggaaacat cagaaccact attttctagc cctctgtcag agcaaacctc agtgcctctc 420
 ctctttgctt gt 432

<210> 126
 <211> 112
 <212> DNA
 <213> Homo sapien

<400> 126
 acacaacttg aatagtataaa tagaaactga gctgaaattt ctaattcact ttctaaccat 60
 agtaagaatg atatttcccc ccagggatca ccaaattttt ataaaaattt gt 112

<210> 127
 <211> 54
 <212> DNA
 <213> Homo sapien

<400> 127
 accacgaaac cacaacaag atggaagcat caatccactt gccaaagcaca gcag 54

<210> 128
 <211> 323
 <212> DNA
 <213> Homo sapien

<400> 128
 acctcattag taattgtttt gttgtttcat ttttttctaa tgtctcccct ctaccagctc 60
 acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgctca 120
 ttctctctga agtctagggt acccattttg gggaccatt ataggcaata aacacagtgc 180
 ccaaagcatt tggacagttt cttgttgtgt tttagaatgg ttttcctttt tcttagcctt 240
 ttcttgcaaa aggctcactc agtcccttgc ttgctcagtg gactgggctc cccagggcct 300
 aggctgcctt cttttccatg tcc 323

<210> 129
 <211> 192
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(192)
 <223> n = A,T,C or G

<400> 129

```

acatacatgt gtgtatatatt ttaaatatca cttttgtatc actctgactt tttagcatac      60
tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc      120
tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg      180
gataaacaaa gt                                     192

```

<210> 130

<211> 362

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(362)

<223> n = A,T,C or G

<400> 130

```

ccctttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca      60
tataatgacg caacaaaaag gtgctgttta gtcctatggt tcagtttatg cccctgacaa      120
gtttccattg tgttttgccg atcttctggc taatcgtggt atcctccatg ttattagtaa      180
ttctgtattc cattttgtta acgcctggta gatgtaacct gctangaggc taactttata      240
cttattttaaa agctcttatt ttgtggatcat taaaatggca atttatgtgc agcactttat      300
tgcagcagga agcacgtgtg gggtgggtgt aaagctcttt gctaattcta aaaagtaatg      360
gg                                     362

```

<210> 131

<211> 332

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 131

```

ctttttgaaa gatcgtgtcc actcctgtgg acatcttggt ttaatggagt ttcccatgca      60
gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaaatgaga      120
gttctcccag gttegccctg ctgctccaag tctcagcagc agcctctttt aggaggcatc      180
ttctgaacta gattaaggca gcttgtaaat ctgatgtgat ttggtttatt atccaactaa      240
cttccatctg ttatcactgg agaaagccca gactccccan gacnggtacg gattgtgggc      300
atanaaggat tgggtgaagc tggcgttgtg gt                                     332

```

<210> 132

<211> 322

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(322)

<223> n = A,T,C or G

<400> 132

```

acttttgcca ttttgtatat ataaacaatc ttgggacatt ctctgaaaa ctaggtgtcc      60

```

```

agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat    120
ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggacctttg tatctcgggt    180
tttagcaagt taaaatgaan atgacaggaa aggccttattt atcaacaaag agaagagttg    240
ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct agggaagcct    300
gtaacaatct acaattgggc ca                                           322

```

<210> 133

<211> 278

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 133

```

acaagccttc acaagtttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt    60
cttgtttttc tttccatctg gtcctgggt tgacaatttg tggaaacaac tctattgcta    120
ctatttaaaa aaaatcacaa atctttccct ttaagctatg ttnaattcaa actattcctg    180
ctattcctgt tttgtcaaag aaattatatt tttcaaaata tgtntatttg tttgatgggt    240
cccacgaac actaataaaa accacagaga ccagcctg                               278

```

<210> 134

<211> 121

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(121)

<223> n = A,T,C or G

<400> 134

```

gtttanaaaa cttgttttagc tccatagagg aaagaatggt aaactttgta ttttaaaaca    60
tgattctctg aggttaaact tggttttcaa atgttatattt tacttgatt ttgcttttgg    120
t                                                                    121

```

<210> 135

<211> 350

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(350)

<223> n = A,T,C or G

<400> 135

```

acttanaacc atgcctagca catcagaatc cctcaaagaa catcagtata atcctatacc    60
atancaagtg gtgactgggt aagcgtgcga caaagggtcag ctggcacatt acttggtgctc    120
aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggtagtcca    180
gggtgcccc caactcctgc agccgctcct ctgtgccagn ccctgnaagg aactttcgct    240
ccacctcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag    300
ttccaagga tgcaaagcct ggtgctcaac tcctggggcg tcaactcagt                350

```

<210> 136
 <211> 399
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (399)
 <223> n = A,T,C or G

<400> 136
 tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt 60
 gctgtgattg tatccgaata ntctcgtga gaaaagataa tgagatgacg tgagcagcct 120
 gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga 180
 cctggcgggc agccagccag ccacaggtgg gcttcttcct tttgtggtga caacnccaag 240
 aaaactgcag agggccaggg tcaggtgtna gtgggtangt gaccataaaa caccaggtgc 300
 tcccaggaac ccgggcaaag gccatcccca cctacagcca gcatgcccac tggcgtgatg 360
 ggtgcagang gatgaagcag ccagntgttc tgcgtggt 399

<210> 137
 <211> 165
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (165)
 <223> n = A,T,C or G

<400> 137
 actggtgtgg tngggggtga tgctgggtgt anaagttgan gtgacttcan gatggtgtgt 60
 ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120
 ttggctggtc cactggtgg tcaactgtcat tgggtggggt cctgt 165

<210> 138
 <211> 338
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (338)
 <223> n = A,T,C or G

<400> 138
 actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc 60
 ttaacttctc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccac 120
 tgctgggcag tctcccatgc cttccacagt gaaagggtt gagaaaaatc acatccaatg 180
 tcatgtgttt ccagccacac caaaaggtgc ttggggtgga gggctggggg catananggt 240
 cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa 300
 aaaaactgat gccttttttt tttttttttg taaaattc 338

<210> 139
 <211> 382

<212> DNA

<213> Homo sapien

<400> 139

gggaatcttg	gtttttggca	tctggtttgc	ctatagccga	ggccactttg	acagaacaaa	60
gaaagggact	tcgagtaaga	aggtgattta	cagccagcct	agtgcccgaa	gtgaaggaga	120
attcaaacag	acctcgtcat	tcctgggtgtg	agcctggtcg	gctcaccgcc	tatcatctgc	180
atttgcccta	ctcaggtgct	accggactct	ggcccctgat	gtctgtagtt	tcacaggatg	240
ccttatttgt	cttctacacc	ccacagggcc	ccctacttct	tcggatgtgt	ttttaataat	300
gtcagctatg	tgccccatcc	tccttcatgc	cctccctccc	tttcctacca	ctgctgagtg	360
gcctggaact	tgtttaaagt	gt				382

<210> 140

<211> 200

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(200)

<223> n = A,T,C or G

<400> 140

accaaantct	ctttctgttg	tgtnngattt	tactataggg	gttnngcttn	ttctaaanat	60
acttttcatt	taacancttt	tgtaagtgt	caggctgcac	tttgctccat	anaattattg	120
ttttcacatt	tcaacttgta	tgtgtttgtc	tcttanagca	ttggtgaaat	cacatatttt	180
atattcagca	taaaggagaa					200

<210> 141

<211> 335

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(335)

<223> n = A,T,C or G

<400> 141

actttatttt	caaaacactc	atatgttgca	aaaaacacat	agaaaaataa	agtttggtgg	60
gggtgctgac	taaacttcaa	gtcacagact	tttatgtgac	agattggagc	agggtttggt	120
atgcatgtag	agaacccaaa	ctaatttatt	aaacaggata	gaaacaggct	gtctgggtga	180
aatggttctg	agaaccatcc	aattcacctg	tcagatgctg	atanactagc	tcttcagatg	240
tttttctacc	agttcagaga	tnggttaatg	actanttcca	atggggaaaa	agcaagatgg	300
attcacaaac	caagtaattt	taaacaaaga	cactt			335

<210> 142

<211> 459

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(459)

<223> n = A,T,C or G

<400> 142
 accagggttaa tattgccaca tatatccttt ccaattgcgg gctaaacaga cgtgtattta 60
 gggttgttta aagacaaccc agcttaatat caagagaaat tgtgacctt catggagtat 120
 ctgatggaga aaacactgag ttttgacaaa tcttatttta ttcagatagc agtctgatca 180
 cacatgggtcc aacaacactc aaataataaa tcaaatatna tcagatgtta aagattgggtc 240
 ttcaaacatc atagccaatg atgcccgcgt tgcctataat ctctccgaca taaaaccaca 300
 tcaacacctc agtggccacc aaaccattca gcacagcttc cttaactgtg agctgtttga 360
 agctaccagt ctgagcacta ttgactatnt ttttcangct ctgaatagct ctagggatct 420
 cagcanggtt gggaggaacc agtcaacct tggcgtaant 459

<210> 143
 <211> 140
 <212> DNA
 <213> Homo sapien

<400> 143
 acatttcctt ccaccaagtc aggactcctg gcttctgtgg gagttcttat cacctgaggg 60
 aaatccaaac agtctctcct agaaaggaat agtgtcacca accccacca tctccctgag 120
 accatccgac ttccctgtgt 140

<210> 144
 <211> 164
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(164)
 <223> n = A,T,C or G

<400> 144
 acttcagtaa caacatacaa taacaacatt aagtgtatat tgccatcttt gtcattttct 60
 atctatacca ctctcccttc tgaaaacaan aatcactanc caatcactta taaaaatttg 120
 aggcaattaa tccatatttg ttttcaataa ggaaaaaaag atgt 164

<210> 145
 <211> 303
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(303)
 <223> n = A,T,C or G

<400> 145
 acgtagacca tccaactttg tatttgtaat ggcaaacatc cagnagcaat tcctaaacaa 60
 actggagggt atttataccc aattatccca ttcattaaca tgccctcttc ctgaggctat 120
 gcaggacagc taccataagt cggcccaggc atccagatac taccatttgt ataaacttca 180
 gttaggggagt ccatccaagt gacaggctta atcaaaggag gaaatggaac ataagcccag 240
 tagtaaaatn ttgcttagct gaaacagcca caaaagactt accgccgtgg tgattaccat 300
 caa 303

<210> 146

<211> 327
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(327)
 <223> n = A,T,C or G

<400> 146
 actgcagctc aattagaagt ggtctctgac ttctcatcanc ttctccctgg gctccatgac 60
 actggcctgg agtgactcat tgctctgggt gggtgagaga gctcctttgc caacaggcct 120
 ccaagtcagg gctgggattt gtttcctttc cacattctag caacaatatg ctggccactt 180
 cctgaacagg gaggggtggga ggagccagca tggacaacagc tgccactttc taaagtagcc 240
 agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgcctgca ggatggaatg 300
 taggggtgag ctgtgtgact ctatgggt 327

<210> 147
 <211> 173
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(173)
 <223> n = A,T,C or G

<400> 147
 acattgtttt tttagataa agcattgana gagctctcct taacgtgaca caatggaagg 60
 actggaacac atacccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120
 atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gtt 173

<210> 148
 <211> 477
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(477)
 <223> n = A,T,C or G

<400> 148
 acaaccactt tatctcatcg aatttttaac ccaaactcac tcaactgtgcc tttctatcct 60
 atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact 120
 gccctactac ctgctgcaat aatcacattc ccttctctgtc ctgaccctga agccattggg 180
 gtggtcctag tggccatcag tccangcctg caccttgagc ccttgagctc cattgctcac 240
 nccanccac ctcaccgacc ccctcctctt acacagctac ctcttgctc tctaacccca 300
 tagattatnt ccaaattcag tcaattaagt tactattaac actctaccog acatgtccag 360
 caccactggg aagccttctc cagccaacac acacacacac acacncacac acacacatat 420
 ccaggcacag gctacctcat cttcacaatc acccctttaa ttaccatgct atgggtgg 477

<210> 149
 <211> 207
 <212> DNA

<213> Homo sapien

<400> 149

acagttgtat tataatatca agaaataaac ttgcaatgag agcatttaag agggaagaac	60
taacgtattt tagagagcca aggaagggtt ctgtggggag tgggatgtaa ggtggggcct	120
gatgataaat aagagtcagc caggtaagtg ggtggtgtgg tatgggcaca gtgaagaaca	180
tttcaggcag agggaacagc agtgaaa	207

<210> 150

<211> 111

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (111)

<223> n = A,T,C or G

<400> 150

accttgattt cattgctgct ctgatggaaa cccaactatc taatttagct aaaacatggg	60
cacttaaatg tggtcagtgt ttggacttgt taactantgg catctttggg t	111

<210> 151

<211> 196

<212> DNA

<213> Homo sapien

<400> 151

agcgcggcag gtcatttga acattccaga tacctatcat tactcgatgc tgttgataac	60
agcaagatgg ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaacat	120
ggataccaac cggaataccc ctatcccga cagcccactg tgggtcccccac tgtctacgag	180
gtgcatccgg ctacgt	196

<210> 152

<211> 132

<212> DNA

<213> Homo sapien

<400> 152

acagcacttt cacatgtaag aaggagaaaa ttcctaaatg taggagaaaag ataacagAAC	60
cttccccttt tcatctagtgt gtggaaacct gatgctttat gttgacagga atagaaccag	120
gaggagagttt gt	132

<210> 153

<211> 285

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (285)

<223> n = A,T,C or G

<400> 153

acaanaccCa nganaggcca ctggccgtgg tgcatggcc tccaaacatg aaagtgtcag	60
--	----

```

cttctgctct tatgtctca tctgacaact ctttaccatt tttatcctcg ctcagcagga      120
gcacatcaat aaagtccaaa gtcttggact tggccttggc ttggaggaag tcatcaacac      180
cctggctagt gaggggtgcg cgccgctcct ggatgacggc atctgtgaag tcgtgcacca      240
gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt                      285

```

<210> 154

<211> 333

<212> DNA

<213> Homo sapien

<400> 154

```

accacagtcc tgttggggcca gggcttcatg accctttctg tgaaaagcca tattatcacc      60
accccaaatt tttccttaaa tatctttaac tgaaggggtc agcctcttga ctgcaaagac      120
cctaagccgg ttacacagct aactccact ggccctgatt tgtgaaattg ctgctgcttg      180
attggcacag gagtcgaagg tggttcagctc cctcctccg tggaacgaga ctctgatttg      240
agtttcacaa attctcgggc cacctcgtca ttgctcctct gaaataaaat ccggagaatg      300
gtcaggcctg tctcatccat atggatcttc cgg                      333

```

<210> 155

<211> 308

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(308)

<223> n = A,T,C or G

<400> 155

```

actggaata ataaaaccca catcacagtg ttgtgtcaaa gatcatcagg gcatggatgg      60
gaaagtgtct tgggaactgt aaagtgccta acacatgata gatgatcttt gttataatat      120
ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggccccag cccagcccc      180
atcacagctc actgctctgt tcatccaggc ccagcatgta gtggctgatt cttcttggct      240
gcttttagcc tccanaagtt tctctgaagc caaccaaacc tctangtgta aggcatgctg      300
gccctggt                      308

```

<210> 156

<211> 295

<212> DNA

<213> Homo sapien

<400> 156

```

acctgtctcg gtgcttggaa catattagga actcaaaata tgagatgata acagtgccta      60
ttattgatta ctgagagaac tgtagacat ttagttgaag attttctaca caggaactga      120
gaataggaga ttatgtttgg cctcatatt ctctcctatc ctcttgcct cattctatgt      180
ctaatatatt ctcaatcaaa taaggtttagc ataatacagga aatcgaccaa ataccaatat      240
aaaaccagat gtctatcctt aagattttca aatagaaaac aaattaacag actat          295

```

<210> 157

<211> 126

<212> DNA

<213> Homo sapien

<400> 157

```

acaagttaa atagtgtgt cactgtgcat gtgctgaaat gtgaaatcca ccacatttct      60

```

gaagagcaaaa acaaattctg tcatgtaatc tctatcttgg gtcgtgggta tatctgtccc 120
cttagt 126

<210> 158
<211> 442
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(442)
<223> n = A,T,C or G

<400> 158
accactgggt cttggaaaca cccatcctta atacgatgat ttttctgtcg tgtgaaaatg 60
aanccagcag gctgccccta gtcagtcctt ccttccagag aaaaagagat ttgagaaagt 120
gcctgggtaa ttcaccatta atttcctccc ccaaactctc tgagtcttcc cttaatatatt 180
ctgggtgggtc tgaccaaagc aggtcatggg ttgttgagca tttgggatcc cagtgaagta 240
natgtttgta gccttgcata cttagccctt cccacgcaca aacggagtg gagagtggg 300
ccaaccctgt tttcccagtc cacgtagaca gattcacagt gcggaattct ggaagctgga 360
nacagacggg ctctttgcag agccgggact ctgagangga catgaggggc tctgcctctg 420
tgttcattct ctgatgtcct gt 442

<210> 159
<211> 498
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(498)
<223> n = A,T,C or G

<400> 159
acttccaggt aacgttggtt tttccgttga gcctgaactg atgggtgacg ttgtagggtc 60
tccaacaaga actgagggtt cagagcgggt aggggaagagt gctgttccag ttgcacctgg 120
gctgctgtgg actgttggtt attcctcact acggcccaag gttgtggaac tggcanaaaag 180
gtgtgtgtgt gganttgagc tcgggcggct gtggtaggtt gtgggctctt caacaggggc 240
tgctgtgggt ccgggangtg aangtggtgt gtcacttgag cttggccagc tctggaaagt 300
antanattct tcctgaaggc cagcgcttgt ggagctggca ngggtcantg ttgtgtgtaa 360
cgaaccagtg ctgctgtggg tgggtgtana tcctccacaa agcctgaagt tatggtgtcn 420
tcaggtaana atgtggtttc agtgtccctg ggcngctgtg gaaggttgta nattgtcacc 480
aagggaataa gctgtggg 498

<210> 160
<211> 380
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(380)
<223> n = A,T,C or G

<400> 160

acctgcatcc agcttccctg ccaaactcac aaggagacat caacctctag acagggaaac 60
agcttcagga tacttccagg agacagagcc accagcagca aaacaaatat tcccatgcct 120
ggagcatggc atagaggaag ctganaaatg tggggtctga ggaagccatt tgagtctggc 180
cactagacat ctcatcagcc acttgtgtga agagatgccc catgacccca gatgcctctc 240
ccacccttac ctccatctca cacacttgag ctttccactc tgtataattc taacatcctg 300
gagaaaaatg gcagtttgac cgaacctgtt cacaacggta gaggctgatt tctaacgaaa 360
cttgtagaat gaagcctgga 380

<210> 161

<211> 114

<212> DNA

<213> Homo sapien

<400> 161

actccacatc cctctgagc aggcggttgt cgttcaaggt gtatttggcc ttgcctgtca 60
cactgtccac tggccctta tccacttggg gcttaatccc tcgaaagagc atgt 114

<210> 162

<211> 177

<212> DNA

<213> Homo sapien

<400> 162

actttctgaa tcgaatcaaa tgatacttag tgtagtttta atatcctcat atatatcaaa 60
gttttactac tctgataatt ttgtaaacca ggtaaccaga acatccagtc atacagcttt 120
tggtgatata taacttggca ataaccagc ctggtgatac ataaaactac tcaactgt 177

<210> 163

<211> 137

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (137)

<223> n = A,T,C or G

<400> 163

catttataca gacaggcgtg aagacattca cgacaaaaac gcgaaattct atcccgtgac 60
canagaaggc agctacggct actcctacat cctggcgtgg gtggccttcg cctgcacctt 120
catcagcggc atgatgt 137

<210> 164

<211> 469

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (469)

<223> n = A,T,C or G

<400> 164

cttatcacia tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta 60
tgcaatgcat catgctatct catacctaag gagggagttc caggagattc aaccaggaaa 120

tgcatggatc	tcaaaggaaa	caaacaccca	ataaactcgg	agtggcagac	tgacaactgt	180
gagacatgca	cttgctacga	aacagaaatt	tcatgttgca	cccttgtttc	tacacctgtg	240
ggttatgaca	aagacaactg	ccaaagaatc	ttcaagaagg	aggactgcaa	gtatatcgtg	300
gtggagaaga	aggacccaaa	aaagacctgt	tctgtcagtg	aatggataat	ctaattgtgct	360
tctagtaggc	acagggctcc	caggccaggc	ctcattctcc	tctggcctct	aatagtcaat	420
gattgtgtag	ccatgcctat	cagtaaaaag	atntttgagc	aaacacttt		469

<210> 165
 <211> 195
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(195)
 <223> n = A,T,C or G

<400> 165	
acagtttttt	atanatatcg
acattgccgg	cacttggtgtt
cagtttcata	aagctgggtg
60	
atccgctgtc	atccactatt
ccttggtctag	agtaaaaatt
attcttatag	cccatgtccc
120	
tgagggccgc	ccgcccgtag
ttctcgttcc	agtcgtcttg
gcacacaggg	tgccaggact
180	
tcctctgaga	tgagt
195	

<210> 166
 <211> 383
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(383)
 <223> n = A,T,C or G

<400> 166	
acatcttagt	agtgtggcac
atcagggggc	catcagggtc
acagtcactc	atagcctcgc
60	
cgaggtcgga	gtccacacca
ccggtgtagg	tgtgctcaat
cttgggcttg	gcgcccacct
120	
ttggagaagg	gatatgctgc
acacacatgt	ccacaaagcc
tgtgaactcg	ccaaagaatt
180	
tttgagacc	agcctgagca
aggggcggat	gttcagcttc
agctcctcct	tcgtcaggtg
240	
gatgccaaac	tcgtctangg
tccgtgggaa	gctgggtgtcc
acntcaccta	caacctgggc
300	
gangatctta	taaagaggct
ccnagataaa	ctccacgaaa
cttctctggg	agctgctagt
360	
nggggccttt	ttggtgaact
ttc	
383	

<210> 167
 <211> 247
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(247)
 <223> n = A,T,C or G

<400> 167	
acagagccag	accttgGCCA
tAAAtgaanc	agagattaag
actaaacccc	aagtcganat
60	
tggagcagaa	actggagcaa
gaagtgggcc	tggggctgaa
gtagagacca	aggccactgc
120	

tatanccata cacagagcca actctcaggc caaggcnatg gttggggcag anccagagac 180
 tcaatctgan tccaaagtgg tggctggaac actggtcatg acanaggcag tgactctgac 240
 tgangtc 247

<210> 168

<211> 273

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(273)

<223> n = A,T,C or G

<400> 168

acttctaagt tttctagaag tggaaggatt gtantcatcc tgaaaatggg tttacttcaa 60
 aatccctcan ccttggttctt cacnactgtc tatactgana gtgtcatgtt tccacaaagg 120
 gctgacacct gagcctgnat ttctactcat ccctgagaag ccctttccag taggggtgggc 180
 aattcccaac ttccttgcca caagcttccc aggcctttctc ccctggaaaa ctccagcttg 240
 agtcccgat acactcatgg gctgccttg gca 273

<210> 169

<211> 431

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(431)

<223> n = A,T,C or G

<400> 169

acagccttg gcttccccaaa ctccacagtc tcagtgcaga aagatcatct tccagcagtc 60
 agctcagacc aggggtcaaag gatgtgacat caacagtttc tggtttcaga acaggttcta 120
 ctactgtcaa atgaccccc atacttctc aaaggctgtg gtaagttttg cacaggtgag 180
 ggcagcagaa aggggggtant tactgatgga caccatcttc tctgtatact ccacactgac 240
 cttgccatgg gcaaaggccc ctaccacaaa aacaatagga tcaactgctgg gcaccagctc 300
 acgcacatca ctgacaaccg ggatggaaaa agaantgcc aacttcatac atccaactgg 360
 aaagtgatct gatactggat tcttaattac cttcaaaaag ttctgggggc catcagctgc 420
 tcgaacactg a 431

<210> 170

<211> 266

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(266)

<223> n = A,T,C or G

<400> 170

acctgtgggc tgggctgtta tgcctgtgcc ggctgctgaa agggagtcca gaggtggagc 60
 tcaaggagct ctgcaggcat tttgccaanc ctctccanag canagggagc aacctacact 120
 ccccgctaga aagacaccag attggagtcc tgggaggggg agttggggtg ggcatttgat 180

gtatacttgt cacctgaatg aangagccag agaggaanga gacgaanatg anattggcct 240
tcaaagctag gggctcggca ggtgga 266

<210> 171

<211> 1248

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1248)

<223> n = A,T,C or G

<400> 171

```

ggcagccaaa tcataaacgg cgaggactgc agcccgcact cgcagccctg gcaggcggca      60
ctgggtcatgg aaaacgaatt gttctgctcg ggcgtcctgg tgcattccga gtgggtgctg      120
tcagccgcac actgtttcca gaagtgagtg cagagctcct acaccatcgg gctgggcctg      180
cacagtcttg aggccgacca agagccaggg agccagatgg tggaggccag cctctccgta      240
cggcacccag agtacaacag acccttgctc gctaacgacc tcatgctcat caagttggac      300
gaatccgtgt ccgagtctga caccatccgg agcatcagca ttgcttcgca gtgccctacc      360
gcggggaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc      420
gtgctgcagt gcgtgaacgt gtcggtggtg tctgaggagg tctgcagtaa gctctatgac      480
ccgctgtacc accccagcat gttctgcgcc ggcggagggc aagaccagaa ggactcctgc      540
aacggtgact ctggggggcc cctgatctgc aacgggtact tgcagggcct tgtgtcttcc      600
ggaaaagccc cgtgtggcca agttggcgtg ccagggtgtct acaccaacct ctgcaaattc      660
actgagtgga tagagaaaac cgtccaggcc agttaactct ggggactggg aacctatgaa      720
attgaccccc aaatacatcc tgcggaagga attcaggaat atctgttccc agccccctct      780
ccctcaggcc caggagtcca ggcccccagc cctcctccc tcaaaccaag ggtacagatc      840
cccagcccct cctccctcag acccaggagt ccagaccccc cagccccctc tccctcagac      900
ccaggagtcc agccccctct cctcagacc caggagtcca gacccccag cccctcctcc      960
ctcagaccga ggggtccagg cccccaacct cctcctccc agactcagag gtccaagccc     1020
ccaaccntc attcccaga cccagaggtc cagggtccag cccctcntcc ctcagaccga     1080
gcggtccaat gccacctaga ctntccctgt acacagtgcc ccttgtggc acgttgaccc     1140
aaccttacca gttggttttt catttttngt ccctttcccc tagatccaga aataaagttt     1200
aagagaagng caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa     1248

```

<210> 172

<211> 159

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(159)

<223> Xaa = Any Amino Acid

<400> 172

```

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
 1              5              10              15
Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
              20              25              30
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
              35              40              45
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
 50              55              60

```


Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
 65 70 75 80
 Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
 85 90 95
 Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
 100 105 110
 Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
 115 120 125
 Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
 130 135 140
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 145 150 155

<210> 173

<211> 1265

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1265)

<223> n = A,T,C or G

<400> 173

```

ggcagcccg c actcgcagcc ctggcaggcg gcactgggtca tggaaaacga attgttctgc      60
tcgggcgtcc tgggtgcatcc gcagtgggtg ctgtcagccg cacactgttt ccagaactcc      120
tacaccatcg ggctgggcct gcacagtctt gaggccgacc aagagccagg gagccagatg      180
gtggaggcca gcctctccgt acggcaccca gagtacaaca gacccttgct cgctaacgac      240
ctcatgctca tcaagttgga cgaatccgtg tccgagtctg acaccatccg gagcatcagc      300
attgcttctg agtgccttac cgcggggaac tcttgccctg tttctggctg gggctctgctg      360
gcgaacggtg agctcacggg tgtgtgtctg ccctcttcaa ggaggtcctc tgcccagtcg      420
cgggggctga cccagagctc tgcgtcccag gcagaatgcc taccgtgctg cagtgcgtga      480
acgtgtcggg ggtgtctgag gaggtctgca gtaagctcta tgaccgctg taccacccca      540
gcatgttctg cggcggcgga gggcaagacc agaaggactc ctgcaacggg gactctgggg      600
ggccctgat ctgcaacggg tacttgaggg gccttggtgc tttcggaaaa gcccgtgtg      660
gccaaagtgg cgtgccaggg gtctacacca acctctgcaa attcactgag tggatagaga      720
aaaccgtcca ggccagttaa ctctggggac tgggaaccca tgaaattgac ccccaaatac      780
atcctgcgga aggaattcag gaatatctgt tcccagcccc tcctccctca ggcccaggag      840
tccaggcccc cagccctctc tccctcaaac caagggtaca gatccccagc ccctcctccc      900
tcagacccag gagtccagac ccccagcccc ctctccctc agaccagga gtccagcccc      960
tcctccntca gaccaggag tccagacccc ccagccctc ctccctcaga ccagggggtt     1020
gaggccccca accctcctc cttcagagtc agaggtccaa gcccacaacc cctcgttccc     1080
cagacccaga ggtnnaggtc ccagccctc ttcntcaga ccagnggtc caatgccacc     1140
tagattttcc ctgnacacag tgcccccttg tggngangttg acccaacctt accagttggg     1200
ttttcatttt tngtcccttt ccctagatc cagaaataaa gtttaagaga nngcaaaaa     1260
aaaaa                                           1265
  
```

<210> 174

<211> 1459

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1459)

<223> n = A,T,C or G

<400> 174

ggtcagccgc	acactgtttc	cagaagtgcg	tgcagagctc	ctacaccatc	gggctggggc	60
tgcacagtct	tgaggccgac	caagagccag	ggagccagat	ggtggaggcc	agcctctccg	120
tacggcacc	agagtacaac	agacccttgc	tcgctaacga	cctcatgctc	atcaagtgg	180
acgaatccgt	gtccgagtct	gacaccatcc	ggagcatcag	cattgcttcg	cagtgccta	240
ccgcggggaa	ctcttgcttc	gtttctggct	ggggtctgct	ggcgaacggt	gagctcacgg	300
gtgtgtgtct	gccctcttca	aggaggtcct	ctgcccagtc	gcgggggctg	accagagct	360
ctgcgctcca	ggcagaatgc	ctaccgtgct	gcagtgcgtg	aacgtgtcgg	tggtgtctga	420
ngaggtctgc	antaagctct	atgaccgct	gtaccacccc	ancatgttct	gcgccggcgg	480
agggcaagac	cagaaggact	cctgcaacgt	gagagagggg	aaaggggagg	gcaggcgact	540
caggggaagg	tggagaagg	ggagacagag	acacacaggg	ccgcatggcg	agatgcagag	600
atggagagac	acacagggag	acagtgacaa	ctagagagag	aaactgagag	aaacagagaa	660
ataaacacag	gaataaagag	aagcaaagga	agagagaaac	agaaacagac	atggggaggc	720
agaaacacac	acacatagaa	atgcagttga	ccttccaaca	gcattggggc	tgaggcggt	780
gacctccacc	caatagaaaa	tcctcttata	acttttgact	ccccaaaaac	ctgactagaa	840
atagcctact	gttgacgggg	agccttacca	ataacataaa	tagtcgattt	atgcatacgt	900
tttatgcatt	catgatatac	ctttgttggg	attttttgat	atttctaagc	tacacagttc	960
gtctgtgaat	ttttttaaat	tgttgcaact	ctcctaaaat	ttttctgatg	tgtttattga	1020
aaaaatccaa	gtataagtgg	acttgtgcat	tcaaaccagg	gttgttcaag	ggtcaactgt	1080
gtaccagag	ggaaacagtg	acacagattc	atagaggtga	aacacgaaga	gaaacaggaa	1140
aaatcaagac	tctacaaaga	ggctgggcag	ggtggctcat	gcctgtaatc	ccagcacttt	1200
gggaggcgag	gcaggcgag	cacttgaggt	aaggagttca	agaccagcct	ggccaaaatg	1260
gtgaaatcct	gtctgtacta	aaaatacaaa	agttagctgg	atatggtggc	aggcgcctgt	1320
aatcccagct	acttgggagg	ctgaggcagg	agaattgctt	gaatatggga	ggcagagggt	1380
gaagtgagtt	gagatcacac	cactatactc	cagctggggc	aacagagtaa	gactctgtct	1440
caaaaaaaaa	aaaaaaaaaa					1459

<210> 175

<211> 1167

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (1167)

<223> n = A,T,C or G

<400> 175

gcgcagccct	ggcaggcgcc	actggtcatg	gaaaacgaat	tgttctgctc	gggcgtcctg	60
gtgcatccgc	agtgggtgct	gtcagccgca	cactgtttcc	agaactccta	caccatcggg	120
ctgggcctgc	acagtcttga	ggccgaccaa	gagccaggga	gccagatggg	ggaggccagc	180
ctctccgtac	ggcaccacga	gtacaacaga	ctcttgctcg	ctaacgacct	catgctcatc	240
aagttggacg	aatccgtgtc	cgagtctgac	accatccgga	gcatacagcat	tgcttcgcag	300
tgccttaccg	cggggaactc	ttgcctcgtn	tctggctggg	gtctgctggc	gaacggcaga	360
atgcctaccg	tgctgcactg	cgtgaacgtg	tcgggtgggt	ctgaggangt	ctgcagtaag	420
ctctatgacc	cgctgtacca	ccccagcatg	ttctgcgccg	gcggaggggc	agaccagaag	480
gactcctgca	acggtgactc	tggggggccc	ctgatctgca	acgggtactt	gcagggcctt	540
gtgtctttcg	gaaaagcccc	gtgtggccaa	cttggcgctg	cagggtgtcta	caccaacctc	600
tgcaaattca	ctgagtggat	agagaaaacc	gtccagncca	gttaactctg	gggactggga	660
acccatgaaa	ttgaccccc	aatacatcct	gcgggaangaa	ttcaggaata	tctgttccca	720
gccctcctc	cctcaggccc	aggagtcag	gccccagcc	cctcctcct	caaaccaagg	780
gtacagatcc	ccagccccct	ctccctcaga	cccaggagtc	cagaccccc	agccctcnt	840
ccntcagacc	caggagtcca	gccctcctc	cntcagacgc	aggagtccag	acccccagc	900

```

centntccg tcagaccag gggcgcaggc cccaacccc tntccntca gagtcagagg      960
tccaagcccc caaccctcg ttccccagac ccagaggtnc aggtcccagc ccctcctccc      1020
tcagaccag cggccaatg ccacctagan tntccctgta cacagtgcgc ccttggtggca      1080
ngttgaccca accttaccag ttgggttttc atttttgtc cctttcccct agatccagaa      1140
ataaagtnta agagaagcgc aaaaaaa                                1167

```

<210> 176
 <211> 205
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(205)
 <223> Xaa = Any Amino Acid

```

<400> 176
Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1          5          10          15
Val Leu Ser Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
      20          25          30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
      35          40          45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
      50          55          60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
      65          70          75          80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
      85          90          95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
      100          105          110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
      115          120          125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
      130          135          140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
      145          150          155          160
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
      165          170          175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
      180          185          190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
      195          200          205

```

<210> 177
 <211> 1119
 <212> DNA
 <213> Homo sapien

```

<400> 177
gcgcactcgc agccctggca ggcggcactg gtcattggaaa acgaattggt ctgctcgggc      60
gtcctgggtgc atccgcagtg ggtgctgtgc gccgcacact gttccagaa ctctacacc      120
atcgggctgg ccctgcacag tcttgaggcc gaccaagacc caggagcca gatggtggag      180
gccagcctct ccgtacggca cccagagtac aacagacct tgctcgctaa cgacctcatg      240
ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct      300

```

```

tcgcagtgcc ctaccgcggg gaactcttgc ctcgtttctg gctgggggtct gctggcgaac   360
gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgatga gaagctttcc   420
caaccctggc agggttgtac catttcggca acttccagtg caaggacgtc ctgctgcatc   480
ctcactgggt gctcactact gctcactgca tcaccggaa cactgtgatc aactagccag   540
caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt   600
actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc   660
cagttatcct cactgaattg agatttcctg cttcagtgtc agccattccc acataatttc   720
tgacctacag aggtgaggga tcatatagct cttcaaggat gctggtactc ccctcacaaa   780
ttcatttctc ctgttgtagt gaaagggtgc cctctggag cctcccaggg tgggtgtgca   840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg   900
ctcagtacac cagggcaggt ctagcatttc ttcatttagt gtatgctgtc cattcatgca   960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg  1020
gaggtgaggg agagggccca tgggtcaatg ggatctgtgc agttgtaaca cattaggtgc  1080
ttaataaaca gaagctgtga tgttaaaaaa aaaaaaaaa  1119

```

<210> 178
 <211> 164
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(164)
 <223> Xaa = Any Amino Acid

<400> 178
 Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1 5 10 15
 Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20 25 30
 Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35 40 45
 Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
 50 55 60
 Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65 70 75 80
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85 90 95
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
 100 105 110
 Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
 115 120 125
 Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
 130 135 140
 Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
 145 150 155 160
 Pro Gly Thr Leu

<210> 179
 <211> 250
 <212> DNA
 <213> Homo sapien

<400> 179

```

ctggagtgcc ttggtgtttc aagccctgc aggaagcaga atgcaccttc tgaggcacct    60
ccagctgccc ccggccgggg gatgcgaggc tcggagcacc cttgcccggc tgtgattgct    120
gccaggcact gttcatctca gcttttctgt ccctttgctc ccggcaagcg cttctgctga    180
aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa    240
aaaaaaaaaa                                     250

```

<210> 180

<211> 202

<212> DNA

<213> Homo sapien

<400> 180

```

actagtccag tgtggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca    60
tcacccagac cccgcccctg cccgtgcccc acgtgctgc taacgacagt atgatgctta    120
ctctgctact cggaaactat ttttatgtaa ttaatgtatg ctttcttggt tataaatgcc    180
tgatttaaaa aaaaaaaaaa aa                                     202

```

<210> 181

<211> 558

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(558)

<223> n = A,T,C or G

<400> 181

```

tccytttgkt naggtttkkg agacamccck agacctwaan ctgtgtcaca gacttcyngg    60
aatgttttagg cagtgcctag aatttcytcg taatgattct gttattactt tcctnattct    120
ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa    180
ggtagtgtga tagtataagt atctaagtgc agatgaaagt gtgttatata tatccattca    240
aaattatgca agtttagtaat tactcagggt taactaaatt actttaatat gctgttgaac    300
ctactctgtt ccttggttag aaaaaattat aaacaggact ttgttagttt gggaagccaa    360
attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw    420
ttttattccc aggaatatgg kgttcatttt atgaatatta cscrggatag awgtwtgagt    480
aaaaycagtt ttggtwaata ygtwaatatg tcmtaaataa acaakgcttt gacttatttc    540
caaaaaaaaa aaaaaaaaaa                                     558

```

<210> 182

<211> 479

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(479)

<223> n = A,T,C or G

<400> 182

```

acagggtttk grggatgcta agsccccrga rwtggtttga tccaaccctg gcttwttttc    60
agaggggaaa atggggccta gaagttacag mscatytagy tggcgcmgtg gcacccctgg    120
cstcacacag astcccagat agctgggact acaggcacac agtcactgaa gcaggccctg    180
ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca    240
ctaagggttaa actttcccac ccagaaaagg caacttagat aaaatcttag agtactttca    300

```

tactmttcta	agtcctcttc	cagcctcact	kkgagtcctm	cytggggggtt	gataggaant	360
ntctcttggc	tttctcaata	aartctctat	ycatctcatg	tttaatttgg	tacgcataara	420
awtgstgara	aaattaaaaat	gttctggtty	inacttttaaaa	araaaaaaaaa	aaaaaaaaa	479

<210> 183

<211> 384

<212> DNA

<213> Homo sapien

<400> 183

aggcgggagc	agaagctaaa	gccaaagccc	aagaagagtg	gcagtgccag	cactggtgcc	60
agtaccagta	ccaataacag	tgccagtgcc	agtgccagca	ccagtgggtg	cttcagtgc	120
gggtgccagcc	tgaccgccac	tctcacattt	gggtctctcg	ctggccttgg	tgagagctggt	180
gccagcacca	gtggcagctc	tggtgcctgt	ggtttctcct	acaagtgaga	ttttagatat	240
tgtaaatcct	gccagtcttt	ctcttcaagc	caggggtgcat	cctcagaaac	ctactcaaca	300
cagcactcta	ggcagccact	atcaatcaat	tgaagttgac	actctgcatt	aratctattt	360
gccattttcaa	aaaaaaaaaa	aaaa				384

<210> 184

<211> 496

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(496)

<223> n = A,T,C or G

<400> 184

accgaattgg	gaccgctggc	ttataagcga	tcatgtyynt	ccrgtatcac	ctcaacgagc	60
agggagatcg	agtctatacg	ctgaagaaat	ttgacccgat	gggacaacag	acctgctcag	120
cccatectgc	tcggtttctc	ccagatgaca	aatactctsg	acaccgaatc	accatcaaga	180
aacgcttcaa	ggtgctcatg	acccagcaac	cgcgcctgt	cctctgaggg	tcccttaaac	240
tgatgtcttt	tctgccacct	gttacccttc	ggagactccg	taaccaaact	cttcggactg	300
tgagccctga	tgcccttttg	ccagccatac	tctttggcat	ccagtctctc	gtggcgattg	360
attatgcttg	tgtgaggcaa	tcatgggtggc	atcacccata	aagggaacac	atttgacttt	420
tttttctcat	attttaaatt	actacmagaw	tattwmagaw	waaatgawtt	gaaaaactst	480
taaaaaaaaa	aaaaaa					496

<210> 185

<211> 384

<212> DNA

<213> Homo sapien

<400> 185

gctggtagcc	tatggcgkgg	cccacggagg	ggctcctgag	gccacggrac	agtgacttcc	60
caagtatcyt	gcgcsgcgtc	ttctaccgtc	cctacctgca	gatcttcggg	cagattcccc	120
aggaggacat	ggacgtggcc	ctcatggagc	acagcaactg	ytcgctcggg	cccggcttct	180
gggcacaccc	tcctggggcc	caggcgggca	cctgcgtctc	ccagtatgcc	aactggctgg	240
tggtgctgct	cctcgctcgc	ttcctgctcg	tgggcaacat	cctgctggtc	aacttgctca	300
ttgccatggt	cagttacaca	ttcggcaaa	tacagggcaa	cagcgatctc	tactgggaag	360
gcgcagcgtt	accgcctcat	ccgg				384

<210> 186

<211> 577

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(577)

<223> n = A,T,C or G

<400> 186

gagtttagctc	ctccacaacc	ttgatgaggt	cgtctgcagt	ggcctctcgc	ttcataccgc	60
tnccatcgtc	atactgtagg	tttgccacca	cytcctggca	tcttggggcg	gcntaatatt	120
ccaggaaact	ctcaatcaag	tcaccgtcga	tgaaacctgt	gggctgggtc	tgtcttccgc	180
tcggtgtgaa	aggatctccc	agaaggagt	ctcgatcttc	cccacacttt	tgatgacttt	240
attgagtcga	ttctgcatgt	ccagcaggag	gttgtaccag	ctctctgaca	gtgaggtcac	300
cagccctatc	atgccgttga	mcgtgccgaa	garcaccgag	ccttgtgtgg	gggkkgaa	360
ctcaccacga	ttctgcatta	ccagagagcc	gtggcaaaag	acattgacaa	actcgcccag	420
gtggaaaaag	amcamctcct	ggargtgctn	gccgctcttc	gtcmgttggt	ggcagcgtw	480
tccttttgac	acacaaacaa	gttaaaggca	ttttcagccc	ccagaaantt	gtcatcatcc	540
aagatntcgc	acagcactna	tccagttggg	attaaat			577

<210> 187

<211> 534

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(534)

<223> n = A,T,C or G

<400> 187

aacatcttcc	tgtataatgc	tgtgtaatat	cgatccgatn	ttgtctgstg	agaatycatw	60
actkggaaaa	gmaacattaa	agcctggaca	ctgggtattaa	aattcacaa	atgcaacact	120
ttaaacagtg	tgtcaatctg	ctcccyynac	tttgtcatca	ccagtctggg	aakaagggtg	180
tgcctatttc	acacctgtta	aaaggcgct	aagcattttt	gattcaacat	cttttttttt	240
gacacaagtc	cgaaaaaagc	aaaagtaaac	agttatyaat	ttgttagcca	attcactttc	300
ttcatgggac	agagccatyt	gatttaaaaa	gcaaattgca	taatattgag	cttygggagc	360
tgatatttga	gcggaagagt	agcctttcta	cttcaccaga	cacaactccc	tttcatattg	420
ggatgttnac	naaagtwatg	tctctwacag	atgggatgct	tttgtggcaa	ttctgttctg	480
aggatctccc	agtttatatta	ccacttgcac	aagaaggcgt	tttcttcttc	agge	534

<210> 188

<211> 761

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(761)

<223> n = A,T,C or G

<400> 188

agaaaccagt	atctctnaaa	acaacctctc	ataccttggt	gacctaat	ttgtgtgcgtg	60
tgtgtgtgcg	cgcataattat	atagacaggc	acatcttttt	tacttttgta	aaagcttatg	120
cctcttttgg	atctatatct	gtgaaagttt	taatgatctg	ccataatgtc	ttggggacct	180

```

ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttngt      240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc ctkgackarg      300
ggggacaaaag aaaagcaaaa ctgamcataa raaacaatwa cctggtgaga arttgcataa      360
acagaaatwr ggtagtatat tgaarnacag catcattaaa rmgttwtktt wttctccctt      420
gcaaaaaaca tgtacngact tcccgttgag taatgccaaag ttgttttttt tatnataaaa      480
cttgcccttc attacatggt tnaaagtggg gtgggtgggcc aaaatattga aatgatggaa      540
ctgactgata aagctgtaca aataagcagt gtgcctaaca agcaacacag taatgttgac      600
atgcttaatt cacaaatgct aatttcatta taaatgtttg ctaaaataca ctttgaacta      660
tttttctgtn ttcccagagc tgagatntta gattttatgt agtatnaagt gaaaaantac      720
gaaaataata acattgaaga aaaaananaaa aaanaaaaaa a                      761

```

```

<210> 189
<211> 482
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(482)
<223> n = A,T,C or G

```

```

<400> 189
tttttttttt ttgcccgatn ctactatttt attgcaggan gtgggggtgt atgcaccgca      60
caccgggggt atnagaagca agaaggaagg agggagggca cagccccttg ctgagcaaca      120
aagccgcctg ctgccttctc tgtctgtctc ctggtgcagg cacatgggga gaccttcccc      180
aaggcagggg ccaccagtcg aggggtggga atacaggggg tgggangtgt gcataagaag      240
tgataggcac aggccacccg gtacagaccc ctccggtcct gacaggtnga ttccgaccag      300
gtcattgtgc cctgcccagg cacagcgtan atctggaaaa gacagaatgc tttccrtttc      360
aaatttggct ngtcatngaa ngggcanttt tccaanttng gctnggtcct ggtaacncttg      420
gttcggccca gtcctncgtc caaaaantat tcaccnncct cnaattgct tgcnggnccc      480
cc                                                                482

```

```

<210> 190
<211> 471
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(471)
<223> n = A,T,C or G

```

```

<400> 190
tttttttttt ttttaaaaca gtttttcaca acaaaattta ttagaagaat agtgggttttg      60
aaaactctcg catccagtga gaactaccat acaccacatt acagctngga atgtnctcca      120
aatgtctggt caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag      180
cgcttttgac atacaatgca caaaaaaaaa aggggggggg gaccacatgg attaaaattt      240
taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt      300
tgaaaaattt catgtatgca atccaaccaa agaacttnat tgggtgatcat gantnctcta      360
ctacatcnac cttgatcatt gccaggaacn aaaagttnaa ancacncngt acaaaaaanaa      420
tctgtaattn anttcaacct ccgtacngaa aaatnttntt tatacactcc c                      471

```

```

<210> 191
<211> 402
<212> DNA

```


<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (402)

<223> n = A,T,C or G

<400> 191

gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct	60
gtcttccact cactgtctgt aagcttttta acccagacwg tatcttcata aatagaacaa	120
attcttcacc agtcacatct tctaggacct ttttgattc agttagtata agctcttcca	180
cttcctttgt taagacttca tctggtaaag tcttaagttt tgtagaaagg aattyaattg	240
ctcgttctct aacaatgtcc tctccttgaa gtatttggct gaacaacca cctaaagtcc	300
ctttgtgcat ccattttaaa tatacttaat agggcattgk tncactaggt taaattctgc	360
aagagtcac tgtctgcaa agttgcgtta gtatatctgc ca	402

<210> 192

<211> 601

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (601)

<223> n = A,T,C or G

<400> 192

gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnnaact	60
ggtctacccc acatgggagc agcatgccgt agntatataa ggctattccc tgagtcagac	120
atgcytyttt gaytaccgtg tgccaagtgc tgggtattct yaacacacyt ccatcccgyt	180
cttttgtgga aaaactggca cttktctgga actagcarga catcacttac aaattcaccc	240
acgagacact tgaaaggtgt aacaaagcga ytcttgcat gctttttgtc cctccggcac	300
cagttgtcaa tactaaccgg ctggtttgcc tccatcacat ttgtgatctg tagctctgga	360
tacatctcct gacagtactg aagaacttct tcttttgttt caaaagcarg tcttggtgcc	420
tggtggatca ggttcccatt tcccagtcyg aatgttcaca tggcatattt wacttcccac	480
aaaacattgc gatttgaggc tcagcaacag caaatcctgt tccggcattg gctgcaagag	540
cctcgatgta gccggccagc gccaaaggcag gcgccgtgag ccccaccagc agcagaagca	600
g	601

<210> 193

<211> 608

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (608)

<223> n = A,T,C or G

<400> 193

atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact	60
ggtcccgcgt tagcccagc gactctccac ctgctggaag cggttgatgc tgcactcytt	120
cccaacgcag gcagmagcgg gscgggtcaa tgaactccay tctggttggtt gggtkgacgg	180
tkaagtgcag gaagaggctg accacctcgc ggccaccag gatgcccgac tgtgcgggac	240
ctgcagcgaa actcctcgat ggcatgagc gggaagcgaa tgaggcccag ggccttgccc	300

```

agaaccttcc gcctgttctc tggcgtcacc tgcagctgct gccgctgaca ctccggcctcg   360
gaccagcgga caaacggcrt tgaacagccg cacctcacgg atgcccagtg tgtcgcgctc   420
caggammgsc accagcgtgt ccagggtcaat gtcggtgaag ccctccgagg gtrattggcg   480
ctgcagtgtt tttgtcgatg ttctccaggc acaggctggc cagctgcggg tcatcgaaga   540
gtcgcgcctg cgtgagcagc atgaaggcgt tgtcggctcg cagttcttct tcagggaactc   600
cacgaat                                         608

```

<210> 194

<211> 392

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (392)

<223> n = A,T,C or G

<400> 194

```

gaacggctgg acctgcctc gcattgtgct tgctggcagg gaataccttg gcaagcagyt   60
ccagtcgag cagccccaga ccgctgccgc ccgaagctaa gcctgcctct ggccttcccc   120
tcgcctcaa tgcagaacca gtagtgggag cactgtgttt agagttaaga gtgaacactg   180
tttgatttta cttgggaatt tcctctgtta tatagctttt cccaatgcta atttccaaac   240
aacaacaaca aaataacatg tttgcctgtt aagttgtata aaagtaggtg attctgtatt   300
taaagaaaat attactgtta catatactgc ttgcaatttc tgtatttatt gktnctstgg   360
aaataaatat agttattaa ggttgtcant cc                                         392

```

<210> 195

<211> 502

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (502)

<223> n = A,T,C or G

<400> 195

```

ccsttkgagg ggtkaggkyc cagttyccga gtggaagaaa caggccagga gaagtgcgtg   60
ccgagctgag gcagatgttc ccacagtgc cccagagacc stgggstata gtytctgacc   120
cctcncaagg aaagaccacs ttctggggac atgggctgga gggcaggacc tagaggcacc   180
aagggaaagg ccattccgg ggstgttccc cgaggaggaa ggggaagggc tctgtgtgcc   240
ccccasgagg aagaggccct gagtcctggg atcagacacc ccttcacgtg tatccccaca   300
caaatgcaag ctcaccaagg tcccctetca gtccccttcc stacacctg amcggccact   360
gscscacacc caccagagc acgccacccg ccatggggar tgtgctcaag gartcgcnng   420
gcarcgtgga catctngtcc cagaagggg cagaatctcc aatagangga ctgarcmstt   480
gctnanaaaa aaaaanaaaa aa                                         502

```

<210> 196

<211> 665

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (665)

<223> n = A,T,C or G

<400> 196

```

ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc      60
cctctggaag ccttgccgag agcggacttt gtaattgttg gagaataact gctgaatttt      120
wagctgtttk gagttgatts gcaccactgc acccacaact tcaatatgaa aacyawttga      180
actwatttat tatcttgtga aaagtataac aatgaaaatt ttgttcatac tgtattkatc      240
aagtatgatg aaaagcaawa gatatatatt cttttattat gttaaattat gattgccatt      300
attaatcggc aaaatgtgga gtgtatgttc ttttcacagt aatatatgcc ttttgtaact      360
tcacttgggt attttattgt aaatgarta caaaattctt aatttaagar aatgggatgt      420
watatttatt tcattaattt ctttcctkgt ttacgtwaat ttgaaaaaga wtgcattgatt      480
tcttgacaga aatcgatctt gatgctgtgg aagtagtttg acccacatcc ctatgagttt      540
ttcttagaat gtataaaggt ttagagccat cnaacttcaa agaaaaaaat gaccacatac      600
tttgcaatca ggctgaaatg tggcatgctn ttctaattcc aactttataa actagcaaan      660
aagtg

```

<210> 197

<211> 492

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(492)

<223> n = A,T,C or G

<400> 197

```

tttntttttt ttttttttgc aggaaggatt ccatttattg tggatgcatt ttcacaatat      60
atgtttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa natttttagg      120
aaggcagatt cacagaacat gctngtcngc ttgcagtttt acctcgatana gatnacagag      180
aattatagtc naaccagtaa acnaggaatt tacttttcaa aagattaaat ccaaactgaa      240
caaaattcta ccttgaaact tactccatcc aaatattgga ataanagtca gcagtgatac      300
attctcttct gaactttaga ttttctagaa aaatatgtaa tagtgatcag gaagagctct      360
tgttcaaaag tacaacnaag caatgttccc ttaccatagg ccttaattca aactttgatc      420
catttcactc ccatcacggg agtcaatgct acctgggaca cttgtatttt gttcatnctg      480
ancntggctt aa

```

<210> 198

<211> 478

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(478)

<223> n = A,T,C or G

<400> 198

```

tttnttttgn atttcantct gtannaanta ttttcattat gtttattana aaaatatnaa      60
tgtntccacn acaaatcatn ttacntnagt aagaggccan ctacattgta caacatacac      120
tgagtatatt ttgaaaagga caagtttaaa gtanacncat attgccganc atancacatt      180
tatacatggc ttgattgata tttagcacag canaaactga gtgagttacc agaaanaaat      240
natatatgtc aatcngattt aagatacaaa acagatccta tggtagatan catcntgtag      300
gagttgtggc tttatgttta ctgaaagtca atgcagttcc tgtacaaaga gatggccgta      360
agcattctag tacctctact ccatgggttaa gaatcgtaac cttatgttta catatgtnta      420

```

gggtaagaat tgtgttaagt naanttattgg agagggtccan gagaaaaatt tgatncaa 478

<210> 199

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(482)

<223> n = A,T,C or G

<400> 199

agtgaacttgt cctccaacaa aaccccttga tcaagtttgt ggcaactgaca atcagaccta	60
tgctagttcc tgcctatctat tcgctactaa atgcagactg gaggggacca aaaaggggca	120
tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga	180
agtgaattcag tttcctctac ggatgagaga ctgggtcaag aatatactca tgcagcttta	240
tgaagccnac tctgaacacg ctggttatct nagatgagaa ncagagaaat aaagtcnaga	300
aaatttacct ggangaaaag aggcctttnng ctggggacca tccattgaa ccttctctta	360
anggacttta agaanaaact accacatgtn tgtngtatcc tgggtgcengg ccggtttantg	420
aacntngacn ncacccctnt ggaatanant cttgaacngcn tctgaactt gctcctctgc	480
ga	482

<210> 200

<211> 270

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(270)

<223> n = A,T,C or G

<400> 200

cgcccgcaag tgcaactcca gctggggccg tgcggacgaa gattctgccca gcagttggtc	60
cgactgcgac gacggcgccg gcgacagtcg caggtgcagc gcggggccct ggggtcttgc	120
aaggctgagc tgacgccgca gaggtcgtgt cacgtccac gaccttgacg ccgtcgggga	180
cagccggaac agagcccggg gaangcggga ggcctcggg agcccctcgg gaagggcggc	240
ccgagagata cgcaggtgca ggtggccgcc	270

<210> 201

<211> 419

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(419)

<223> n = A,T,C or G

<400> 201

tttttttttt ttttgaatc tactgcgagc acagcaggtc agcaacaagt ttattttgca	60
gctagcaagg taacagggta gggcatggtt acatgttcag gtcaacttcc tttgtcgtgg	120
ttgattggtt tgtctttatg ggggcggggg ggggtagggg aaancgaagc anaantaaca	180
tggagtgggt gcaccctccc tgtagaacct gggtacnaaa gcttggggca gttcacctgg	240

<223> n = A,T,C or G

<400> 204

ttttttttnt	tttttttttt	tttttttntc	ttcttttttt	ttganaatga	ggatcgagtt	60
tttcaactct	tagatagggc	atgaagaaaa	ctcatctttc	cagcttttaa	ataacaatca	120
aatctcttat	gctatatcat	attttaagtt	aaactaatga	gtcactggct	tatcttctcc	180
tgaaggaaat	ctgttcattc	ttctcattca	tatagttata	tcaagtacta	ccttgcatat	240
tgagaggttt	ttcttctcta	tttacacata	tatttccatg	tgaatttgta	tcaaaccctt	300
attttcatgc	aaactagaaa	ataatgtntt	cttttgcata	agagaagaga	acaatatnag	360
cattacaaaa	ctgctcaaat	tgtttggtta	gnttatccat	tataattagt	tnggcaggag	420
ctaatacaaa	tcacattttac	ngacnagcaa	taataaaaact	gaagtaccag	ttaaatatcc	480
aaaataatta	aaggaacatt	tttagcctgg	gtataattag	ctaattcact	ttacaagcat	540
ttattnagaa	tgaattcaca	tggtattatt	ccntagccca	acacaatgg		589

<210> 205

<211> 545

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(545)

<223> n = A,T,C or G

<400> 205

tttttntttt	ttttttcagt	aataatcaga	acaatattta	tttttatatt	taaaattcat	60
agaaaagtgc	cttacattta	ataaaagttt	gtttctcaaa	gtgatcagag	gaattagata	120
tngtcttgaa	caccaatatt	aatttgagga	aaatacacca	aaatacatta	agtaaattat	180
ttaagatcat	agagcttgta	agtgaaaaaga	taaaatttga	cctcagaaac	tctgagcatt	240
aaaaatccac	tattagcaaa	taaattacta	tggacttctt	gctttaattt	tgtgatgaat	300
atgggggtgc	actggtaaac	caacacattc	tgaaggatac	attacttagt	gatagattct	360
tatgtacttt	gctanatnac	gtggatatga	gttgacaagt	ttctctttct	tcaatctttt	420
aaggggcnag	ngaaatgagg	aagaaaagaa	aaggattacg	catactgttc	tttctatngg	480
aaggattaga	tatgttttct	ttgccaatat	taaaaaaata	ataatgttta	ctactagtga	540
aaccc						545

<210> 206

<211> 487

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(487)

<223> n = A,T,C or G

<400> 206

tttttttttt	tttttttagtc	aagtttctna	tttttattat	aattaaagtc	ttgggtcattt	60
catttattag	ctctgcaact	tacatatatta	aattaaagaa	acgttnttag	acaactgtna	120
caatttataa	atgtaagggtg	ccattattga	gtanatatat	tcctccaaga	gtggatgtgt	180
ccttctctcc	accaactaat	gaancagcaa	cattagttta	attttattag	tagatnatac	240
actgtgcaa	acgctaattc	tcttctccat	ccccatgtng	atattgtgta	tatgtgtgag	300
ttggtnagaa	tgcatcanca	atctnacaat	caacagcaag	atgaagctag	gcntgggctt	360
tcggtgaaaa	tagactgtgt	ctgtctgaat	caaagatct	gacctatcct	cgggtggcaag	420
aactcttcga	accgcttctt	caaaggcngc	tgccacattt	gtggcntctn	ttgcacttgt	480

ttcaaaa

487

<210> 207

<211> 332

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 207

tgaattggct	aaaagactgc	atTTTTanaa	ctagcaactc	ttatttcttt	cctttaaaaa	60
tacatagcat	taaattccaa	atcctattta	aagacctgac	agcttgagaa	ggtcactact	120
gcatttatag	gaccttctgg	tggttctgct	gttacntttg	aantctgaca	atccttgana	180
atctttgcat	gcagaggagg	taaaaggtat	tggtttttca	cagaggaana	acacagcgca	240
gaaatgaagg	ggccaggctt	actgagcttg	tccactggag	ggctcatggg	tggtgacatgg	300
aaaagaaggc	agcctaggcc	ctggggagcc	ca			332

<210> 208

<211> 524

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(524)

<223> n = A,T,C or G

<400> 208

agggcggtgt	gcggagggcg	ttactgtttt	gtctcagtaa	caataaatac	aaaaagactg	60
gttggtgtcc	ggcccatcc	aaccacgaag	ttgatttctc	ttgtgtgcag	agtgactgat	120
tttaaaggac	atggagcttg	tcacaatgtc	acaatgtcac	agtggtgaagg	gcacactcac	180
tcccgcgtga	ttcacattta	gcaaccaaca	atagctcatg	agtccatact	tgtaaatact	240
tttggcagaa	tacttnttga	aacttgacga	tgataactaa	gatccaagat	atttcccaaa	300
gtaaatagaa	gtgggtcata	atattaatta	cctgttcaca	tcagcttcca	tttacaagtc	360
atgagcccag	acactgacat	caaactaagc	ccacttagac	tcctcaccac	cagtctgtcc	420
tgatcatcaga	caggaggctg	tcaccttgac	caaattctca	ccagtcaatc	atctatccaa	480
aaaccattac	ctgatccact	tccggtaatg	caccaccttg	gtga		524

<210> 209

<211> 159

<212> DNA

<213> Homo sapien

<400> 209

gggtgaggaa	atccagagtt	gcatggaga	aaattccagt	gtcagcattc	ttgctccttg	60
tggccctctc	ctacactctg	gccagagata	ccacagtcaa	acctggagcc	aaaaaggaca	120
caaaggactc	tcgacccaaa	ctgccccaga	ccctctcca			159

<210> 210

<211> 256

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(256)
 <223> n = A,T,C or G

<400> 210
 actccctggc agacaaaggc agaggagaga gctctgtag ttctgtgtg ttgaactgcc 60
 actgaatttc tttccacttg gactattaca tgccanttga gggactaatg gaaaaacgta 120
 tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgggagagat 180
 ttgcagggtg naaatgggan ggctggtttg ttanatgaac agggacatag gaggtaggca 240
 ccaggatgct aaatca 256

<210> 211
 <211> 264
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(264)
 <223> n = A,T,C or G

<400> 211
 acattgtttt tttagataa agcattgaga gagctctect taacgtgaca caatggaagg 60
 actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120
 atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gttaaggaga 180
 ggggagatac attcngaaag aggactgaaa gaaatactca agtnggaaaa cagaaaaaga 240
 aaaaaaggag caaatgagaa gcct 264

<210> 212
 <211> 328
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(328)
 <223> n = A,T,C or G

<400> 212
 acccaaaaat ccaatgctga atatttggtc tcattattcc canattcttt gattgtcaaa 60
 ggatttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag 120
 gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccgccag 180
 ttnaatttca ttccattga cttgggatcc ttatcatcag ccagagagat tgaaaattta 240
 cccctacnac tctttactct ctgganaggg ccagtgggtg tagctataag cttggccaca 300
 ttttttttct ctttattcct ttgtcaga 328

<210> 213
 <211> 250
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1) ... (250)

<223> n = A,T,C or G

<400> 213

acttatgagc	agagcgacat	atccnagtgt	agactgaata	aaactgaatt	ctctccagtt	60
ttaaagcattg	ctcactgaag	ggatagaagt	gactgccagg	agggaaagta	agccaaggct	120
cattatgccca	aagganatat	acatttcaat	tctccaaact	tcttcctcat	tccaagagtt	180
ttcaatatatt	gcatgaacct	gctgataanc	catgttaana	aacaaatata	tctctnacct	240
tctcatcggt						250

<210> 214

<211> 444

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (444)

<223> n = A,T,C or G

<400> 214

accagaaatc	caatgctgaa	tatttggtct	cattattccc	agattctttg	attgtcaaag	60
gatttaattg	tgtctcagct	tgggcacttc	agttaggacc	taaggatgcc	agccggcagg	120
tttatatatg	cagcaacaat	attcaagcgc	gacaacaggt	tattgaactt	gcccggcagg	180
tgaatttcat	tccattgac	ttgggatcct	tatcatcagc	canagagatt	gaaaatttac	240
ccctacgact	ctttactctc	tggagagggc	cagtgggtgt	agctataagc	ttggccacat	300
ttttttttcc	ttttattcct	tgtcagagat	gcgattcatc	catatgctan	aaaccaacag	360
agtgactttt	acaaaattcc	tataganatt	gtgaataaaa	ccttacctat	agttgccatt	420
actttgctct	ccctaataata	cctc				444

<210> 215

<211> 366

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (366)

<223> n = A,T,C or G

<400> 215

acttatgagc	agagcgacat	atccaagtgt	anactgaata	aaactgaatt	ctctccagtt	60
ttaaagcattg	ctcactgaag	ggatagaagt	gactgccagg	agggaaagta	agccaaggct	120
cattatgccca	aagganatat	acatttcaat	tctccaaact	tcttcctcat	tccaagagtt	180
ttcaatatatt	gcatgaacct	gctgataagc	catgttgaga	aacaaatata	tctctgacct	240
tctcatcggt	aagcagaggc	tgtaggcaac	atggaccata	gcgaanaaaa	aacttagtaa	300
tccaagctgt	tttctacact	gtaaccaggt	ttccaaccaa	ggtggaaatc	tcctatactt	360
ggtgcc						366

<210> 216

<211> 260

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(260)
 <223> n = A,T,C or G

<400> 216
 ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgtc 60
 caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctnttnc atttttttat 120
 taataaaaag tnnaaaaggc ctcttctcaa cttttttccc ttnggctgga aaatttaaaa 180
 atcaaaaatt tcctnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240
 aattcttcct tccttccttt 260

<210> 217
 <211> 262
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(262)
 <223> n = A,T,C or G

<400> 217
 acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta 60
 tcttgccat atttttctat ttttaataagg aaatagcaaa ttgggggtggg gggaatgtag 120
 ggcattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180
 atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta 240
 atatccttca tgcttgtaaa gt 262

<210> 218
 <211> 205
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(205)
 <223> n = A,T,C or G

<400> 218
 accaaggtgg tgcattaccg gaantggatc aangacacca tcgtggccaa cccctgagca 60
 cccctatcaa ctcccttttg tagtaaaactt ggaaccttgg aaatgaccag gccaaagactc 120
 aggcctcccc agttctactg acctttgtcc ttangtntna ngcccagggt tgctaggaaa 180
 anaaatcagc agacacaggt gtaaa 205

<210> 219
 <211> 114
 <212> DNA
 <213> Homo sapien

<400> 219
 tactgttttg tctcagtaac aataaatata aaaagactgg ttgtgttccg gccccatcca 60
 accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220
 <211> 93

<212> DNA

<213> Homo sapien

<400> 220

actagccagc acaaaaggca gggtagcctg aattgctttc tgctctttac atttctttta	60
aaataagcat ttagtgctca gtccctactg agt	93

<210> 221

<211> 167

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (167)

<223> n = A,T,C or G

<400> 221

actangtgca ggtgcgacaca aatatttgct gatattccct tcattcttga ttccatgagg	60
tcttttgccc agcctgtggc tctactgtag taagtctctg ctgatgagga gccagnatgc	120
ccccactac cttccctgac gctcccana aatcacccaa cctctgt	167

<210> 222

<211> 351

<212> DNA

<213> Homo sapien

<400> 222

agggcgtggt gcgaggggcg gtactgacct cattagtagg aggatgcatt ctggcacccc	60
gttcttcacc tgtcccccaa tccttaaaag gccatactgc ataaagtcaa caacagataa	120
atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa	180
ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt	240
taggtgagca tgattagaga gctttagagt tgcttttaca tatatctggc atatttgagt	300
ctcgtatcaa aacaatagat tggtaaaggt ggtattattg tattgataag t	351

<210> 223

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (383)

<223> n = A,T,C or G

<400> 223

aaaacaaaca acaaaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat	60
tggttaattat ggtcaattta atwrtrttkt ggggcatttc cttacattgt cttgacaaga	120
ttaaaaatgct tgtgccaaaa ttttgatttt tatttggaga cttcttatca aaagtaatgc	180
tgccaaagga agtctaagga attagtagtg ttcccmcac ttgtttggag tgtgctattc	240
taaaagattt tgatttcctg gaatgacaat tatattttta ctttggtggg ggaaanagtt	300
ataggaccac agtcttcact tctgatactt gtaaattaat cttttattgc acttgttttg	360
accattaagc tatatgttta aaa	383

<210> 224

<211> 320
 <212> DNA
 <213> Homo sapien

<400> 224
 cccctgaagg cttcttggtta gaaaatagta cagttacaac caataggaac aacaaaaaga 60
 aaaagtttgt gacattgttag tagggagtgt gtacccctta ctcccatca aaaaaaaat 120
 ggatacatgg ttaaaggata raagggaat attttatcat atgttctaaa agagaaggaa 180
 gagaaaatac tactttctcr aaatggaagc ccttaaagggt gctttgatac tgaaggacac 240
 aaatgtggcc gtccatctc ctttaragtt gcatgacttg gacacggtaa ctgttgcaat 300
 tttaractcm gcattgtgac 320

<210> 225
 <211> 1214
 <212> DNA
 <213> Homo sapien

<400> 225
 gaggactgca gcccgactc gcagccctgg caggcggcac tggatcatgga aaacgaattg 60
 ttctgctcgg gcgtcctggt gcatccgcag tgggtgctgt cagccgcaca ctgtttccag 120
 aactcctaca ccacgggct gggcctgcac agtcttgagg ccgaccaaga gccagggagc 180
 cagatggtgg agggcagcct ctccgtacgg caccagagt acaacagacc ctgtctcgt 240
 aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtctgacac catccggagc 300
 atcagcattg ctccgcagtg ccctaccgcg gggaactctt gcctcgtttc tggctgggggt 360
 ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg tgaacgtgtc ggtggtgtct 420
 gaggaggtct gcagtaagct ctatgaccgc ctgtaccacc ccagcatgtt ctgcgcgggc 480
 ggagggcaag accagaagga ctctgcaac ggtgactctg gggggcccct gatctgcaac 540
 gggtaacttg agggccttgt gtctttcgga aaagccccgt gtggccaagt tggcgtgcca 600
 ggtgtctaca ccaacctctg caaattcact gagtggatag agaaaaccgt ccaggccagt 660
 taactctggg gactgggaac ccataaatt gacccccaa tacatcctgc ggaaggaatt 720
 caggaatata tgttcccagc ccctcctccc tcaggccag gagtccagg cccagcccc 780
 tcctccctca aaccaagggt acagatcccc agccccctct ccctcagacc caggagtcca 840
 gacccccag ccctcctcc ctccagacca ggagtccagc ccctcctccc tcagaccag 900
 gagtccagac cccccagccc ctccctccc agaccagggt gtccaggccc ccaaccctc 960
 ctccctcaga ctccagagtc caagcccca accctcctt cccagaccc agaggtccag 1020
 gtcccagccc ctccctccc agaccagcg gtccaatgcc acctagactc tcctgttaca 1080
 cagtgtcccc ttgtggcacg ttgacccaac cttaccagtt gggttttcat ttttgtccc 1140
 tttccctag atccagaaat aaagtctaag agaagcgcaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaaaaaaaa aaaa 1214

<210> 226
 <211> 119
 <212> DNA
 <213> Homo sapien

<400> 226
 acccagtatg tgcagggaga cggaaccca tgtgacagcc cactccacca gggttcccaa 60
 aagacctggc ccagtcataa tcattcatcc tgacagtggc aataatcacg ataaccagt 119

<210> 227
 <211> 818
 <212> DNA
 <213> Homo sapien

<400> 227

acaattcata	gggacgacca	atgaggacag	ggaatgaacc	cggctctccc	ccagccctga	60
tttttgctac	atatggggtc	ccttttcatt	ctttgcaaaa	acactgggtt	ttctgagaac	120
acggacgggt	cttagacaaa	tttgtgaaat	ctgtgtaraa	ccgggctttg	caggggagat	180
aattttcctc	ctctggagga	aaggtggtga	ttgacaggca	gggagacagt	gacaaggcta	240
gagaaagcca	cgctcggcct	tctctgaacc	aggatggaac	ggcagacccc	tgaaaacgaa	300
gcttgtcccc	ttccaatcag	ccacttctga	gaaccccat	ctaacttctt	actggaaaag	360
agggcctcct	caggagcagt	ccaagagttt	tcaaagataa	cgtgacaact	accatctaga	420
ggaaaagggtg	caccctcagc	agagaagccg	agagcttaac	tctggtcgtt	tccagagaca	480
acctgctggc	tgtcttgga	tgcgccagc	ctttgagagg	ccactacccc	atgaacttct	540
gccatccact	ggcatgaag	ctgaggacac	tgggcttcaa	caactgagttg	tcatgagagg	600
gacaggctct	gccctcaagc	cggctgaggg	cagcaaccac	tctcctcccc	tttctcacgc	660
aaagccattc	ccacaaatcc	agaccatacc	atgaagcaac	gagacccaaa	cagtttggct	720
caagaggata	tgaggactgt	ctcagcctgg	ctttgggctg	acaccatgca	cacacacaag	780
gtccacttct	aggttttcag	cctagatggg	agtcgtgt			818

<210> 228

<211> 744

<212> DNA

<213> Homo sapien

<400> 228

actggagaca	ctgttgaact	tgatcaagac	ccagaccacc	ccagggtctcc	ttcgtgggat	60
gtcatgacgt	ttgacatacc	tttggaacga	gcctcctcct	tggaaatgg	aagaccgtgt	120
tcgtggccga	cctggcctct	cctggcctgt	ttcttaagat	gcggagtcac	atttcaatgg	180
taggaaaagt	ggcttcgtaa	aatagaagag	cagtcactgt	ggaactacca	aatggcgaga	240
tgctcgggtc	acattggggg	gctttgggat	aaaagattta	tgagccaact	attctctggc	300
accagattct	aggccagttt	gttccactga	agcttttccc	acagcagtc	acctctgcag	360
gctggcagct	gaatggcttg	ccgggtggctc	tgtggcaaga	tcacactgag	atcgatgggt	420
gagaaggcta	ggatgcttgt	ctagtgttct	tagctgtcac	gttggctcct	tccagggttg	480
ccagacgggtg	ttggccactc	ccttctaaaa	cacaggcgcc	ctcctggtga	cagtgaacctg	540
ccgtgggtatg	ccttggccca	ttccagcagt	cccagttatg	catttcaagt	ttgggggttg	600
ttcttttctg	taatgttctt	ctgtgttgtc	agctgtcttc	atttctggg	ctaagcagca	660
ttgggagatg	tggaccagag	atccactcct	taagaaccag	tggcgaaaga	cactttcttt	720
cttcaactctg	aagtagctgg	tggt				744

<210> 229

<211> 300

<212> DNA

<213> Homo sapien

<400> 229

cgagtctggg	ttttgtctat	aaagtttgat	ccctcctttt	ctcatccaaa	tcattgtgaac	60
cattacacat	cgaaataaaa	gaaagggtgc	agacttgccc	aacgccaggc	tgacatgtgc	120
tgcagggttg	ttgtttttta	attattattg	ttagaaacgt	caccacagct	ccctgttaac	180
ttgtatgtga	cagccaactc	tgagaaggtc	ctatttttcc	acctgcagag	gatccagctc	240
cactaggctc	ctccttgccc	tcacactgga	gtctccgcca	gtgtgggtgc	ccactgacat	300

<210> 230

<211> 301

<212> DNA

<213> Homo sapien

<400> 230

cagcagaaca	aatacaata	tgaagagtgc	aaagatctca	taaaatctat	gctgaggaat	60
gagcgacagt	tcaaggagga	gaagcttgca	gagcagctca	agcaagctga	ggagctcagg	120

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caatataaag tcctgggtca cactcaggaa cgagagctga cccagttaag ggagaagttg      180
cggaagggga gagatgcctc cctctcattg aatgagcatc tccaggccct cctcactccg      240
gatgaaccgg acaagtccca ggggcaggac ctccaagaaa cagacctcgg ccgcgaccac      300
g                                                                                   301

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<210> 231
<211> 301
<212> DNA
<213> Homo sapien

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<400> 231
gcaagcacgc tggcaaatct ctgtcaggtc agctccagag aagccattag tcatttttagc      60
caggaactcc aagtccacat ccttggcaac tggggacttg cgcaggttag ccttgaggat      120
ggcaacacgg gacttctcat caggaagtgg gatgtagatg agctgatcaa gacggccagg      180
tctgaggatg gcaggatcaa tgatgtcagg ccggttggtg ccgccaatga tgaacacatt      240
tttttttggt gacatgccat ccatttctgt caggatctgg ttgatgactc ggtcagcagc      300
c                                                                                   301

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<210> 232
<211> 301
<212> DNA
<213> Homo sapien

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<400> 232
agtaggtatt tcgtgagaag ttcaacacca aaactggaac atagttctcc ttcaagtgtt      60
ggcgacagcg gggcttcctg attctggaat ataactttgt gtaaattaac agccacctat      120
agaagagtc atctgctgtg aaggagagac agagaactct gggttccgtc gtcctgtcca      180
cgtgctgtac caagtgtctg tgccagcctg ttacctgttc tcaactgaaaa tctggctaatt      240
gctctgtgtg atcacttctg attctgacaa tcaatcaatc aatggcctag agcactgact      300
g                                                                                   301

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<210> 233
<211> 301
<212> DNA
<213> Homo sapien

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<400> 233
atgactgact tcccagtaag gctctctaag gggtaagtag gaggatccac aggatttgag      60
atgctaaggc cccagagatc gtttgatcca accctcttat ttccagaggg gaaaatgggg      120
cctagaagtt acagagcatc tagctggtgc gctggcacc ctaggcctcac acagactccc      180
gagtagctgg gactacaggc acacagtcac tgaagcaggc cctgttagca attctatgcg      240
tacaaattaa catgagatga gttagagactt tattgagaaa gcaagagaaa atcctatcaa      300
c                                                                                   301

```

```

<210> 234
<211> 301
<212> DNA
<213> Homo sapien

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```

<400> 234
aggtcctaca catcgagact catccatgat tgatatgaat ttaaaaatta caagcaaaga      60
cattttattc atcatgatgc tttcttttgt ttcttctttt cgttttcttc tttttctttt      120
tcaatttcag caacatactt ctcaatttct tcaggattta aaatcttgag ggattgatct      180
cgctcatga cagcaagttc aatgtttttg ccacctgact gaaccacttc caggagtgcc      240
ttgatcacca gcttaatggg cagatcatct gcttcaatgg cttcgtcagt atagttcttc      300

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t		301
<210>	235	
<211>	283	
<212>	DNA	
<213>	Homo sapien	
<400>	235	
tggggctgtg catcaggcgg gtttgagaaa tattcaattc tcagcagaag ccagaatttg	60	
aattccctca tcttttaggg aatcatttac caggtttgga gaggattcag acagctcagg	120	
tgctttcact aatgtctctg aacttctgtc cctctttggt catggatagt ccaataaata	180	
atgttatctt tgaactgatg ctcataggag agaataaag aactctgagt gatatcaaca	240	
ttagggattc aaagaaatat tagatttaag ctcacactgg tca	283	
<210>	236	
<211>	301	
<212>	DNA	
<213>	Homo sapien	
<400>	236	
aggtcctcca ccaactgcct gaagcacggg taaaattggg aagaagtata gtgcagcata	60	
aatactttta aatcgatcag atttccctaa cccacatgca atcttcttca ccagaagagg	120	
tcggagcagc atcattaata ccaagcagaa tgcgtaatag ataaatacaa tggatatatag	180	
tgggtagacg gcttcatgag tacagtgtac tgtggtatcg taatctggac ttgggttgta	240	
aagcatcgtg taccagtcag aaagcatcaa tactcgacat gaacgaatat aaagaacacc	300	
a	301	
<210>	237	
<211>	301	
<212>	DNA	
<213>	Homo sapien	
<400>	237	
cagtggtagt ggtggtggac gtggcggttg tcgtggtgcc ttttttggtg cccgtcacia	60	
actcaatttt tggtcgctcc tttttggcct tttccaattt gtccatctca attttctggg	120	
ccttggtcaa tgctcatag taggagtcct cagaccagcc atggggatca aacatatcct	180	
ttgggtagtt ggtgccaagc tcgtcaatgg cacagaatgg atcagcttct cgtaaattca	240	
gggttccgaa attctttctt cctttggata atgtagttca tatccattcc ctctttatc	300	
t	301	
<210>	238	
<211>	301	
<212>	DNA	
<213>	Homo sapien	
<400>	238	
gggcagggtt tttttttttt ttttttgatg gtgcagaccc ttgctttatt tgtctgactt	60	
gttcacagtt cagccccctg ctcaaaaaac caacgggcca gctaaggaga ggaggaggca	120	
ccttgagact tccggagtcg aggtcttcca gggttcccca gccatcaat cattttctgc	180	
acccctgcc tgggaagcag ctccctgggg ggtgggaatg ggtgactaga agggatttca	240	
gtgtgggacc cagggtctgt tcttcacagt aggaggtgga agggatgact aatttcttta	300	
t	301	
<210>	239	
<211>	239	

<212> DNA

<213> Homo sapien

<400> 239

ataagcagct agggaattct ttatttagta atgtcctaac ataaaagtgc acataactgc	60
ttctgtcaaa ccatgatact gagctttgtg acaaccaga aataactaag agaaggcaaa	120
cataatacct tagagatcaa gaaacattta cacagttcaa ctgtttaaaa atagctcaac	180
attcagccag tgagtagagt gtgaatgcc aacatacacag tatacaggtc cttcaggga	239

<210> 240

<211> 300

<212> DNA

<213> Homo sapien

<400> 240

ggtcctaattg aagcagcagc ttccacattt taacgcaggt ttacggtgat actgtccttt	60
gggatctgcc ctccagtga accctttaag gaagaagtgg gcccaagcta agttccacat	120
gctgggtgag ccagatgact tctgttcctt ggtcactttc ttcaatgggg cgaatggggg	180
ctgccaggtt tttaaaatca tgcttcatct tgaagcacac ggtcacttca cctcctcac	240
gctgtgggtg tactttgatg aaaataccca ctttgttggc ctttctgaag ctataatgtc	300

<210> 241

<211> 301

<212> DNA

<213> Homo sapien

<400> 241

gaggctcgtt gctgaggtct ctgggctagg aagaggagtt ctgtggagct ggaagccaga	60
cctctttgga ggaaactcca gcagctatgt tgggtgtctt gagggaaatgc aacaaggctg	120
ctcctccatg tattggaaaa ctgcaaaactg gactcaactg gaaggaagtg ctgctgccag	180
tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agtcttttct	240
tcctcctcct gtcatacggg ctctctcaag catcctttgt tgtcaggggc ctaaaaggga	300
g	301

<210> 242

<211> 301

<212> DNA

<213> Homo sapien

<400> 242

ccgaggtcct gggatgcaac caatcactct gtttcacgtg acttttatca ccatacaatt	60
tgtggcattt cctcattttc tacattgtag aatcaagagt gtaaataaat gtatatcgat	120
gtcttcaaga atatatcatt cttttttcac tagaaccat tcaaaatata agtcaagaat	180
cttaatatca acaaatatat caagcaaact ggaaggcaga ataactacca taatttagta	240
taagtaccca aagttttata aatcaaaagc cctaatagata accattttta gaattcaatc	300
a	301

<210> 243

<211> 301

<212> DNA

<213> Homo sapien

<400> 243

aggtaagtcc cagtttgaag ctcaaaagat ctggtatgag cataggctca tcgacgacat	60
gggtggcccaa gctatgaaat cagagggagg cttcatctgg gcctgtaaaa actatgatgg	120

tgacgtgcag tcggactctg tggcccaagg gtatggctct ctcggcacga tgaccagcgt	180
gctggtttgt ccagatggca agacagtaga agcagaggct gccacggga ctgtaacccg	240
tcactaccgc atgttccaga aaggacagga gacgtccacc aatcccattg cttccatttt	300
t	301

<210> 244

<211> 300

<212> DNA

<213> Homo sapien

<400> 244

gctggtttgc aagaatgaaa tgaatgattc tacagctagg acttaacctt gaaatggaaa	60
gtcatgcaat cccatttgca ggatctgtct gtgcacatgc ctctgtagag agcagcattc	120
ccagggacct tggaaacagt tgacactgta aggtgcttgc tccccaagac acatcctaaa	180
aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc cttctctatt tatgtgaaca	240
actgttgtc ttttgtgtat cttttttaa ctgtaaagt caattgtgaa aatgaatattc	300

<210> 245

<211> 301

<212> DNA

<213> Homo sapien

<400> 245

gtctgagtat ttaaaatggt attgaaatta tccccaacca atgttagaaa agaaagaggt	60
tataactta gataaaaaat gaggtgaatt actatccatt gaaatcatgc tcttagaatt	120
aaggccagga gatattgtca ttaatgtara cttcaggaca cttagagtata gcagccctat	180
gttttcaaag agcagagatg caattaaata ttgttttagca tcaaaaaggc cactcaatac	240
agctaataaa atgaaaagacc taatttctaa agcaattctt tataattttac aaagttttaa	300
g	301

<210> 246

<211> 301

<212> DNA

<213> Homo sapien

<400> 246

ggtctgtcct acaatgcctg cttcttgaaa gaagtcggca ctttctagaa tagctaaata	60
acctgggctt attttaaaga actatttgta gctcagattg gttttcctat ggctaaaata	120
agtgttctt gtgaaaatta aataaaacag ttaattcaaa gccttgatat atgttaccac	180
taacaatcat actaaatata ttttgaagta caaagtttga catgctctaa agtgacaacc	240
caaagtgtgc ttacaaaaca cgttcctaac aaggtatgct ttacactacc aatgcagaaa	300
c	301

<210> 247

<211> 301

<212> DNA

<213> Homo sapien

<400> 247

aggtcctttg gcagggtcga tggatcagag ctcaaactgg agggaaaggc atttcgggta	60
gcctaagagg gcgactggcg gcagcacaac caagggaaggc aagggtgttt cccccagct	120
gtgtcctgtg ttcagggtcg acacacaatc ctcatgggaa caggatcac catgctgtgc	180
ccttgatgat caaggttggg gcttaagtgg attaaggag gcaagtctg gggtccttgc	240
cttttcaaac catgaagtca ggctctgtat cctcctttt cctaactgat attctaacta	300
a	301

<210> 248
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 248
 aggtccttgg agatgccatt tcagccgaag gactcttctw ttcggaagta caccctcact 60
 attaggaaga ttcttagggg taatttttct gaggaaggag aactagccaa cttagaatt 120
 acaggaagaa agtggtttgg aagacagcca aagaaataaa agcagattaa attgtatcag 180
 gtacattcca gctgttggc aactccataa aaacatttca gattttaatc ccgaatttag 240
 ctaatgagac tggatttttg ttttttatgt tgtgtgtcgc agagctaaaa actcagttcc 300
 c 301

<210> 249
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 249
 gtccagagga agcacctggg gctgaactag gcttgccctg ctgtgaactt gcacttggag 60
 ccctgacgct gctgttctcc ccgaaaaacc cgaccgaact ccgcgatctc cgtcccgccc 120
 ccaggagagac acagcagtga ctcagagctg gtcgcacact gtgcctccct cctcaccgcc 180
 catcgtaatg aattattttg aaaattaatt ccaccatcct ttcagattct ggatggaaag 240
 actgaatctt tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt 300
 a 301

<210> 250
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 250
 ggtctgtgac aaggacttgc aggctgtggg aggcaagtga cccttaacac tacacttctc 60
 cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc 120
 cataagcaca tcagtacttt tctctggctg gaatagtaaa ctaaagtatg gtacatctac 180
 ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta 240
 caataaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc 300
 a 301

<210> 251
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 251
 gccgaggtec tacatttggc ccagtttccc cctgcaccc ctccagggcc cctgcctcat 60
 agacaacctc atagagcata ggagaactgg ttgccctggg gccaggggga ctgtctggat 120
 gccagggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct 180
 cattgggatc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccgga 240
 cctctggagg ggggcagtgg aatcccagct ccaggacgga tctgttcgaa aagatatcct 300
 c 301

<210> 252
 <211> 301

<212> DNA

<213> Homo sapien

<400> 252

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gcaaccaatc actctgtttc acgtgacttt taccaccata caatttgttg catttcctca      60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtctt caagaatata      120
tcatttccttt ttcactagga acccattcaa aatataagtc aagaatctta atatcaacaa      180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag taccctaaagt      240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc      300
a                                                                                   301
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<210> 253

<211> 301

<212> DNA

<213> Homo sapien

<400> 253

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ttccctaaga agatgttatt ttgttgggtt ttgttcccc tccatctcga ttctcgtacc      60
caactaaaaa aaaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctcccttagct      120
tggtctgatt gttttcagac cttaaaatat aaacttggtt cacaagcttt aatccatgtg      180
gatttttttt cttagagaac cacaaaacat aaaaggagca agtcggactg aatacctgtt      240
tccatagtgc ccacagggtg ttcctcacat tttctccata ggaaaatgct ttttcccaag      300
g                                                                                   301
```

<210> 254

<211> 301

<212> DNA

<213> Homo sapien

<400> 254

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cgctgcgcct ttcccttggg ggagggggcaa ggccagaggg ggtccaagtg cagcacgagg      60
aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaaatcccc      120
ccaaatctct tcatcttacc ctggtggact cctgactgta gaattttttg gttgaaacaa      180
gaaaaaaata aagctttgga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc      240
acttaaacct agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc      300
t                                                                                   301
```

<210> 255

<211> 302

<212> DNA

<213> Homo sapien

<400> 255

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agcttttttt tttttttttt tttttttttt ttcattaaaa aatagtgtct tttattataa      60
attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagtt tgacttggat      120
tggtgatttt ttgagtctct caagcatctc ctaataccct caagggcctg agtagggggg      180
aggaaaaagg actggagggt gaatctttat aaaaaacaag agtgattgag gcagattgta      240
aacattatta aaaaacaaga acaaaacaaa aaaaatagaga aaaaaaccac cccaacacac      300
aa                                                                                   302
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<210> 256

<211> 301

<212> DNA

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 256
gttccagaaa acattgaagg tggcttccca aagtctaact agggatcccc cctctagcct 60
aggaccctcc tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc 120
acccccaaaa gcctggacac cttgagcaca cagttatgac caggacagac tcatctctat 180
aggcaaatag ctgctggcaa actggcatta cctggttttgt ggggatgggg gggcaagtgt 240
gtggcctctc ggcttggtta gcaagaacat tcagggtagg cctaagttan tcgtgttagt 300
t 301

<210> 257
<211> 301
<212> DNA
<213> Homo sapien

<400> 257
gttgtggagg aactctggct tgctcattaa gtcctactga ttttactat cccctgaatt 60
tccccactta tttttgtctt tcaactatcg aggccttaga agaggctctac ctgcctccag 120
tcttacctag tccagtctac cccctggagt tagaatggcc atcctgaagt gaaaagtaat 180
gtcacattac tcccttcagt gatttcttgt agaagtgcc atccctgaat gccaccaaga 240
tcttaatctt cacatcttta atcttatctc tttgactcct ctttacaccg gagaaggctc 300
c 301

<210> 258
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 258
cagcagtagt agatgccgta tgccagcacg cccagcactc ccaggatcag caccagcacc 60
aggggcccag ccaccaggcg cagaagcaag ataaacagta ggctcaagac cagagccacc 120
cccagggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat cttaacactg 180
atgtctcggg cattgaggct gtcaataana cgctgatccc ctgctgtatg gtggtgtcat 240
tgggtgatccc tgggagcgcc ggtggagtaa cgttgggtcca tggaaagcag cgcccacaac 300
t 301

<210> 259
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 259

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tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg    60
gtgtcctgaa gtgatttgga cccctgaggg cagacaccta agtaggaatc ccagtgggaa    120
gcaaagccat aaggaagccc aggattcctt gtgatcagga agtgggccag gaaggtctgt    180
tccagctcac atctcatctg catgcagcac ggaccggatg cgcccactgg gtcttggctt    240
ccctcccac ttctcaagca gtgtccttgt tgagccattt gcatecttgg ctccagggtg    300
c

```

<210> 260

<211> 301

<212> DNA

<213> Homo sapien

<400> 260

```

tttttttct ccctaaggaa aaagaaggaa caagtctcat aaaaccaa at aagcaatggt    60
aaggtgtctt aacttgaaaa agattaggag tcaactggtt acaagttata attgaatgaa    120
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaaca caggattaac    180
tagggcaaaa taaataagtg tgtggaagcc ctgataagtg cttaataaac agactgattc    240
actgagacat cagtacctgc ccgggcggcc gtcgagccg aattctgcag atatccatca    300
c

```

<210> 261

<211> 301

<212> DNA

<213> Homo sapien

<400> 261

```

aaatattcga gcaaattctg taactaatgt gtctccataa aaggctttga actcagtga    60
tctgcttcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaagggt    120
agcaccaact attccatata attcatcagc aggaaataaa ggctcttcag aaggttcaat    180
ggtgacatcc aattttcttct gataatttag attcctcaca acctcctag ttaagtgaag    240
ggcatgatga tcatccaaag ccagtggtc acttactcca gactttctgc aatgaagatc    300
a

```

<210> 262

<211> 301

<212> DNA

<213> Homo sapien

<400> 262

```

gaggagagcc tggtacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc    60
tgtgagcttc ttgccgcaag tctctcagaa atttaaaaag atgcaaatcc ctgagtcacc    120
cctagacttc ctaaaccaga tcctctgggg ctggaacctg gcaactctga tttgtaatga    180
gggctttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtgcc    240
catcattacc cccacattat aatgggatag attcagagca gatactctcc agcaaagaat    300
c

```

<210> 263

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (301)

<223> n = A,T,C or G

<400> 263

tttagcttgt ggtaaatgac tcacaaaact gatttttaaaa tcaagttaat gtgaattttg	60
aaaattacta cttaatccta attcacaata acaatggcat taaggtttga cttgagttgg	120
ttcttagtat tatttatggg aaataggctc ttaccacttg caaataactg gccacatcat	180
taatgactga cttcccagta aggctctcta aggggtaagt angaggatcc acaggatttg	240
agatgctaag gccccagaga tcgtttgatc caaccctctt attttcagag gggaaaatgg	300
g	301

<210> 264

<211> 301

<212> DNA

<213> Homo sapien

<400> 264

aaagacgtta aaccactcta ctaccacttg tggaactctc aaagggtaaa tgacaaascc	60
aatgaatgac tctaaaaaca atattttacat ttaatggttt gtagacaata aaaaaacaag	120
gtggatagat ctagaattgt aacattttta gaaaaccata scatttgaca gatgagaaaag	180
ctcaattata gatgcaaagt tataactaaa ctactatagt agtaaagaaa tacatttcac	240
acccttcata taaattcact atcttggett gaggcactcc ataaaatgta tcacgtgcat	300
a	301

<210> 265

<211> 301

<212> DNA

<213> Homo sapien

<400> 265

tgcccaagtt atgtgtaagt gtatccgcac ccagaggtaa aactacactg tcattctttgt	60
cttcttgatga cgcagtattt cttctctggg gagaagccgg gaagtcttct cctggctcta	120
catattcttg gaagtctcta atcaactttt gttccatttg tttcatttct tcaggaggga	180
ttttcagttt gtcaacatgt tctctaaca cacttgccca tttctgtaaa gaatccaaag	240
cagtccaagg ctttgacatg tcaacaacca gcataactag agtatccttc agagatacgg	300
c	301

<210> 266

<211> 301

<212> DNA

<213> Homo sapien

<400> 266

taccgtctgc ctttctctcc atccaggcca tctgcgaatc tacatgggtc ctctatttcg	60
acaccagatc actctttcct ctaccacag gcttgctatg agcaagagac acaacctcct	120
ctcttctgtg ttccagcttc ttttctgtt cttcccaccc cttaagttct attcctgggg	180
atagagacac caatacccat aacctctctc ctaagcctcc ttataacca ggggtgcacag	240
cacagactcc tgacaactgg taaggccaat gaactgggag ctcacagctg gctgtgctg	300
a	301

<210> 267

<211> 301

<212> DNA

<213> Homo sapien

<400> 267

aaagagcaca ggccagctca gcctgccctg gccatctaga ctcagcctgg ctccatgggg	60
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gtttctcagtg ctgagtcctat ccaggaaaaag ctcacctaga ccttctgagg ctgaatcttc 120
atcctcacag gcagcttctg agagcctgat attcctagcc ttgatggctt ggagtaaagc 180
ctcattctga ttctctcct tcttttcttt caagttggct ttctcacat cctctgttc 240
aatcgcttc agcttgctg ctttagccct cattccaga agcttcttct ctttggcatc 300
t 301

<210> 268
<211> 301
<212> DNA
<213> Homo sapien

<400> 268
aatgtctac tcaactactt cccagcctac cgtggcctaa ttctgggagt tttcttctta 60
gatcttggga gagctggttc ttctaaggag aaggaggaag gacagatgta actttggatc 120
tcgaagagga agtctaattg aagtaattag tcaacggctc ttgttttagac tcttggaata 180
tgctgggtgg ctcagtgagc ccttttggag aaagcaagta ttattcttaa ggagtaacca 240
cttccattg ttctactttc taccatcatc aattgtatat tatgtattct ttggagaact 300
a 301

<210> 269
<211> 301
<212> DNA
<213> Homo sapien

<400> 269
taacaatata cactagctat ctttttaact gtccatcatt agcaccaatg aagattcaat 60
aaaattacct ttattcacac atctcaaaac aattctgcaa attcttagtg aagtttaact 120
atagtcacag accttaaata ttacattgt tttctatgtc tactgaaaat aagttcacta 180
cttttctgga tattctttac aaaatcttat taaaattcct ggtattatca cccccaatta 240
tacagtagca caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc 300
t 301

<210> 270
<211> 301
<212> DNA
<213> Homo sapien

<400> 270
cattgaagag cttttgcgaa acatcagaac acaagtgcct ataaaattaa ttaagcctta 60
cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga 120
gagcttgctg gtgcagtgca tattggataa cactattcat ggccgaattg atcaagtcaa 180
ccaactcctt gaactggatc atcagaagaa ggggtggtgca cgatatactg cactagataa 240
tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggctt aacagaaaac 300
a 301

<210> 271
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)... (301)
<223> n = A,T,C or G

<400> 271

```

aaaaggttct cataagatta acaattttaa taaatatttg atagaacatt ctttctcatt      60
tttatagctc atcttttaggg ttgatattca gttcatgctt cccttgctgt tcttgatcca    120
gaattgcaat cacttcatca gcctgtattc gctccaattc tctataaagt ggggtccaagg    180
tgaaccacag agccacagca cacctctttc ccttggtgac tgccttcacc ccatganggt    240
tctctcctcc agatganaac tgatcatgcg cccacatttt gggttttata gaagcagtc      300
c

```

301

<210> 272

<211> 301

<212> DNA

<213> Homo sapien

<400> 272

```

taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaattgc      60
ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga    120
tccaataatt ccctcatgat gagcaagaaa aattctttgc gcacccctcc tgcattccaca    180
gcatctttct caacaaatat aaccttgagt ggcttcttgt aatctatgtt ctttgttttc    240
ctaaggactt ccattgcatc tcctacaata ttttctctac gcaccactag aattaagcag    300
g

```

301

<210> 273

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (301)

<223> n = A,T,C or G

<400> 273

```

acatgtgtgt atgtgtatct ttgggaaaaa aanaagacat cttgtttayt atttttttgg      60
agagangctg ggacatggat aatcacwtaa tttgctayta tyactttaat ctgactygaa    120
gaaccgtcta aaaataaaat ttaccatgtc dtatattcct tatagtatgc ttatttcacc    180
tlytttctgt ccagagagag tatcagtgtc ananatttma ggggtgaamac atgmattggg    240
gggacttnty tttacngagm accctgcccg sgcgcctcg makcngantt ccgcsananc    300
t

```

301

<210> 274

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (301)

<223> n = A,T,C or G

<400> 274

```

cttatatact ctttctcaga ggcaaaagag gagatgggta atgtagacaa ttctttgagg      60
aacagtaaat gattattaga gagaangaat ggaccaagga gacagaaatt aacttgtaaa    120
tgattctctt tggaatctga atgagatcaa gaggccagct ttagcttggt gaaaagtcca    180
tctaggtatg gttgcattct cgtcttcttt tctgcagtag ataatgaggt aaccgaaggc    240
aattgtgctt cttttgataa gaagctttct tggatcatatc aggaaattcc aganaaagtc    300

```

301

c

301

<210> 275
 <211> 301
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 275

tcggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg	60
gggtgaaatt ggccaacttt ctattaactt atgttggtgcaa ttttgccacc aacagtaagc	120
tggtcccttct aataaaagaa aattgaaagg tttctcacta aacggaatta agtagtggag	180
tcaagagact ccagggcctc agcgtacctg ccggggcggc cgctcgaagc cgaattctgc	240
agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgccctat	300
a	301

<210> 276
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 276

tgtacacata ctcaataaat aaatgactgc atttgtgtat tattactata ctgattatat	60
ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tatacaaaat	120
taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc	180
caatacatctt aaacatttgg gaaatgaggg ggacaaatgg aagccagatc aaatttgtgt	240
aaaactattc agtatgttcc ccttgcttca tgtctgagaa ggctctcctt caatggggat	300
g	301

<210> 277
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 277

tttgttgatg tcagtattttt attacttgcg ttatgagtgc tcacctggga aattctaaag	60
atacagagga cttggaggaa gcagagcaac tgaatttaat ttaaaagaag gaaaacattg	120
gaatcatggc actcctgata ctttcccaaa tcaacactct caatgcccc aacctgtcct	180
caccatagtg gggagactaa agtggccacg gatttgcctt angtgtgcag tgcgttctga	240
gttcnctgtc gattacatct gaccagtctc ctttttccga agtccttccg ttcaatcttg	300
c	301

<210> 278
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 278
 taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60
 aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgtca 120
 cagtctctac tgttattatg cattacctgg gaatttatat aagcccttaa taataatgcc 180
 aatgaacatc tcatgtgtgc tcacaatgtt ctggcactat tataagtgc tccacaggtt 240
 tatgtgttct tcgtaacttt atggantagg tactcggccg cgaacacgct aagccgaatt 300
 c 301

<210> 279
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 279
 aaagcaggaa tgacaaagct tgcttttctg gtatgttcta ggtgtattgt gacttttact 60
 gttatatata ttgccaatat aagtaaata agattatata tgtatagtgt ttcacaaagc 120
 ttagaccttt accttcacag caccacacag tgcttgatat ttcagagtca gtcattgggt 180
 atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240
 catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300
 a 301

<210> 280
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 280
 ggtactggag ttttctccc ctgtgaaaac gtaactactg ttgggagtga attgaggatg 60
 tagaaagggt gtggaaccaa attgtggtca atggaaatag gagaatatgg ttctcactct 120
 tgagaaaaaa acctaaagatt agcccaggta gttgcctgta acttcagttt ttctgcctgg 180
 gtttgatata gtttaggggt ggggttagat taagatctaa attacatcag gacaaagaga 240
 cagactatta actccacagt taattaagga ggtatgttcc atgtttattt gttaaagcag 300
 t 301

<210> 281
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 281
 aggtacaaga aggggaatgg gaaagagctg ctgctgtggc attgttcaac ttggatatcc 60
 gccgagcaat ccaaactctg aatgaagggg catcttctga aaaaggagat ctgaatctca 120
 atgtggtagc aatggcttta tcgggttata cggatgagaa gaactccctt tggagagaaa 180
 tgtgtagcac actgcgatta cagctaaata acccgatatt gtgtgtcatg ttgcatcttc 240

tgacaagtga aacaggatct tacgatggag ttttgtatga aaacaaagtt gcagtacctc 300
g 301

<210> 282
<211> 301
<212> DNA
<213> Homo sapien

<400> 282
caggtactac agaattaaaa tactgacaag caagtagttt cttggcgtgc acgaattgca 60
tccagaacct aaaaattaag aaattcaaaa agacattttg tgggcacctg ctagcacaga 120
agcgcagaag caaagcccag gcagaacctat gtaacctta cagctcagcc tgcacagaag 180
cgcagaagca aagcccaggc agaaccatgc taaccttaca gctcagcctg cacagaagcg 240
cagaagcaaa gccccaggcag aacatgctaa ccttacagct cagcctgcac agaagcacag 300
a 301

<210> 283
<211> 301
<212> DNA
<213> Homo sapien

<400> 283
atctgtatag ggcagacaaa ctttatarag tgtagagagg tgagcgaaag gatgcaaaag 60
cactttgagg gctttataat aatatgctgc ttgaaaaaaa aaatgtgtag ttgatactca 120
gtgcatctcc agacatagta aggggttgct ctgaccaatc aggtgatcat tttttctatc 180
acttcccagg ttttatgcaa aaattttgtt aaattctata atggtgatat gcattcttta 240
ggaaacatat acatttttaa aaatctattt tatgtaagaa ctgacagacg aatttgcttt 300
g 301

<210> 284
<211> 301
<212> DNA
<213> Homo sapien

<400> 284
caggtacaaa acgctattaa gtggccttaga atttgaacat ttgtggtctt tatttacttt 60
gcttcgtgtg tgggcaaagc aacatcttcc cttaaataat attaccaaga aaagcaagaa 120
gcagattagg tttttgacaa acaaacagg ccaaaagggg gctgacctgg agcagagcat 180
ggtgagaggc aaggcatgag agggcaagtt tggtgtggac agatctgtgc ctactttatt 240
actggagtaa aagaaaacaa agttcattga tgtcgaagga tatatacagt gttagaaatt 300
a 301

<210> 285
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 285
acatcaccat gatcggtacc cccacccatt atacgttgta tgtttacata aatactcttc 60
aatgatcatt agtgttttaa aaaaaatact gaaaactcct tctgcacccc aatctctaac 120

caggaaagca aatgctatctt acagacctgc aagccctccc tcaaacnaaa ctatttctgg 180
attaaatatt tctgacttct tttaggttca cagcactagg caaatgctat ttacgatctg 240
caaaagctgt ttgaagagtc aaagcccca tgtgaacacg atttctggac cctgtaacag 300
t 301

<210> 286

<211> 301

<212> DNA

<213> Homo sapien

<400> 286

taccactgca ttccagcctg ggtgacagag tgagactccg tctccaaaaa aaactttgct 60
tgtatattat ttttgcccta cagtggatca ttctagtagg aaaggacagt aagatttttt 120
atcaaaatgt gtcatgccag taagagatgt tatattcttt tctcatttct tccccacca 180
aaaataagct accatatagc ttataagtct caaatttttg ccttttacta aaatgtgatt 240
gtttctgttc attgtgtatg cttcatcacc tatattaggc aaattccatt ttttcccttg 300
t 301

<210> 287

<211> 301

<212> DNA

<213> Homo sapien

<400> 287

tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg 60
cccagaagga acgtagagat cagatattac aacagctttg ttttgagggg tagaaatatg 120
aaatgatttg gttatgaacg cacagttagg gcagcagggc cagaatcctg accctctgcc 180
ccgtggttat ctctcccca gcttggctgc ctcatgttat cacagtattc ctttttgttt 240
gttgcattgc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggtaatgc 300
t 301

<210> 288

<211> 301

<212> DNA

<213> Homo sapien

<400> 288

gtacacctaa ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag 60
agtcaatagg aagacaaatt ccagttccag ctcatctggg gtatctgcaa agctgcaaaa 120
gatctttaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatac 180
aaaagcatct gcttttgtga ttttaatttag ctcatctggc cactggaaga atccaaacag 240
tctgccttaa ttttggatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300
a 301

<210> 289

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 289

ggtacactgt	tccatgtta	tgtttctaca	cattgctacc	tcagtgtcc	tggaaactta	60
gcttttgatg	tctccaagta	gtccaccttc	atttaactct	ttgaaactgt	atcatctttg	120
ccaagtaaga	gtggtggcct	atttcagctg	ctttgacaaa	atgactggct	cctgacttaa	180
cgttctataa	atgaatgtgc	tgaagcaaag	tgcccatggg	ggcggcgaan	aagagaaaaga	240
tgtgttttgt	tttgactct	ctgtgggtccc	ttccaatgct	gtgggtttcc	aaccagnnga	300
a						301

```
<210> 290
<211> 301
<212> DNA
<213> Homo sapien
```

```
<220>  
<221> misc_feature  
<222> (1)...(301)  
<223> n = A,T,C or G
```

<400>	290	
acactgagct	cttcttgata	aatatacaga atgcttgga tatacaagat tctatactac 60
tgactgatct	gttcatttct	ctcacagctc ttaccccca aagcttttcc accctaagtg 120
ttctgacctc	cttttcta	atcacagtagg atagaggcag anccacctac aatgaacatg 180
gagttctatc	aagaggcaga	aacagcacag aatcccgatt ttaccattcg ctagcagtg 240
tgccctgaac	aaaaacattt	ctccatgtct cattttcttc atgcctcaag taacagtgag 300
a		301

```
<210> 291
<211> 301
<212> DNA
<213> Homo sapien
```

<400>	291	
caggtagcaaa	tttcttctat	cctagaaaca
tatatcagct	agattttttt	tctatgcttt
tttactcttt	tgtttatagg	tgaatcacaa
agccatggct	gtttacttca	tttaatttat
acatgagctt	cacttcccca	ctaactaatt
a		

```
<210> 292
<211> 301
<212> DNA
<213> Homo sapien
```

```
<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G
```

<400> 292						
accttttagt	agtaatgtct	aataataaat	aagaaatcaa	ttttataagg	tccatatagc	60
tgtattaaat	aatttttaag	tttaaaagat	aaaataccat	catttttaaat	gttggtattc	120
aaaaccaaag	natataaccg	aaaggaaaaa	cagatgagac	ataaaatgat	ttgcnagatg	180
ggaaatatag	tasttyatga	atgtnatta	aattccagtt	ataatagtgg	ctacacactc	240
tcactacaca	cacagacccc	acagtcctat	atgccacaaa	cacattttcca	taacttgaaa	300
a						301

<210> 293
<211> 301
<212> DNA
<213> Homo sapien

<400> 293
ggtaccaagt gctgggtgcc gctgtttacc tgtttctcact gaaaagtctg gctaattgctc 60
ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggccctagagc actgactgtt 120
aacacaaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaa gctgtttctgt 180
gtgagaattt tttaaaaggc tacttgtata ataacccttg tcatttttaa tgtacctcgg 240
ccgcgaccac gctaagccga attctgcaga tatccatcac actggcggcc gctcgagcat 300
g 301

<210> 294
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 294
tgaccataaa caatatacac tagctatctt ttttaactgtc catcattagc accaatgaag 60
attcaataaa attaccttta ttcacacatc tcaaaaacaat tctgcaaatt cttagtgaag 120
tttaactata gtcacaganc ttaaatattc acattgtttt ctatgtctac tgaaaataag 180
ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc 240
cccaattata cagtagcaca accaccttat gtagttttta catgatatgt ctgtagaggt 300
t 301

<210> 295
<211> 305
<212> DNA
<213> Homo sapien

<400> 295
gtactctttc tctccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta 60
cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac 120
ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga 180
actggtagaa aaacrtctga agagctagtc tatcagcatc tgacaggtga attggatggt 240
tctcagaacc atttcaccca gacagcctgt ttctatcctg ttttaataaat tagtttgggt 300
tctct 305

<210> 296
<211> 301
<212> DNA
<213> Homo sapien

<400> 296
aggtagctatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct 60
cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg 120
attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac 180
tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt 240

tgtcattact ataaatttta aaatctgtta ataagatggc ctataggag gaaaaagggg 300
c 301

<210> 297
<211> 300
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(300)
<223> n = A,T,C or G

<400> 297
actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta 60
aaggttttga aaaccttgaa ggagaatcat ttgacaaga agtacttaag agtctagaga 120
acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt 180
tccatcattg ggagtgcact ggccatccct caaaatttgt ctgggctggc ctgagtgggc 240
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc aactggcgg 300

<210> 298
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 298
tatggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc ccctcccgcg 60
ggcatctgag agacctgggtg ttccagtgtt tctggaaatg ggtcccagtg ccgccggctg 120
tgaagctctc agatcaatca cgggaagggc ctggcggtgg tggccacctg gaaccacct 180
gtcctgtctg ttacatttc actaycaggt tttctctggg cattacnatt tgttccccta 240
caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcaggtggct ctcagcgagg 300
t 301

<210> 299
<211> 301
<212> DNA
<213> Homo sapien

<400> 299
gttttgagac ggagtttcac tcttgttgcc cagactggac tgcaatggca ggttctctgc 60
tactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct cccaggtagc 120
tggtattgca ggctcagcc accataccca gctaattttt ttgtattttt agtagagacg 180
gagtttcgcc atgttgcca gctgggtctca aactcctgac ctcaagcgac ctgcctgcct 240
cgccctccca aagtgtgga attataggca tgagtcaaca cgccagcct aaagatatatt 300
t 301

<210> 300
<211> 301
<212> DNA
<213> Homo sapien

<400> 300

```

attcagtttt atttgctgcc ccagtatctg taaccaggag tgccacaaaa tcttgccaga    60
tatgtcccac acccactggg aaaggctccc acctggctac ttcctctatc agctgggtca    120
gctgcattcc acaaggttct cagcctaata agtttacta cctgccagtc tcaaaactta    180
gtaaagcaag accatgacat tccccacgg aaatcagagt ttgccccacc gtcttggtac    240
tataaagcct gcctctaaca gtccttgctt cttcacacca atcccgagcg catcccccat    300
g

```

301

<210> 301

<211> 301

<212> DNA

<213> Homo sapien

<400> 301

```

ttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagtctgc    60
agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagttagt    120
gggaactcac aaagaccctc agagctgaga caccacaaac agtgggagct cacaagacc    180
ctcagagctg agacaccac aacagtggga gtcacaaaag accctcagag ctgagacacc    240
cacaacagca cctcgttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt    300
t

```

301

<210> 302

<211> 301

<212> DNA

<213> Homo sapien

<400> 302

```

aggtacacat ttagcttggt gtaaagtact cacaaaactg attttaaaat caagttaatg    60
tgaattttga aaattactac ttaatcctaa ttcacaataa caatggcatt aaggtttgac    120
ttgagttggg tcttagtatt atttatggta aataggctct taccacttgc aaataactgg    180
ccacatcatt aatgactgac ttcccagtaa ggctctctaa ggggtaagta ggaggatcca    240
caggatttga gatgctaagg ccccagagat cgtttgatcc aaccctctta ttttcagagg    300
g

```

301

<210> 303

<211> 301

<212> DNA

<213> Homo sapien

<400> 303

```

aggtaccaac tgtggaaata ggtagaggat ctttttttct ttccatatca actaagttgt    60
atattgtttt ttgacagttt aacacatctt cttctgtcag agattctttc acaatagcac    120
tggctaattg aactaccgct tgcattgtaa aaatgggtgg ttgtgaaatg atcataggcc    180
agtaacgggt atgtttttct aactgatctt ttgctcgttc caaagggacc tcaagacttc    240
catcgatttt atatctgggg tctagaaaag gagttaatct gttttccctc ataaattcac    300
c

```

301

<210> 304

<211> 301

<212> DNA

<213> Homo sapien

<400> 304

```

acatggatgt tattttgcag actgtcaacc tgaatttgta tttgcttgac attgcctaatt    60

```



```

tattagtttc agtttcagct tacccacttt ttgtctgcaa catgcaraas agacagtgcc      120
cttttttagtg tatcatatca ggaatcatct cacattgggtt tgtgccatta ctggtgcagt      180
gacttttcagc cacttgggta aggtggagtt ggccatatgt ctccactgca aaattactga      240
ttttcctttt gtaattaata agtgtgtgtg tgaagattct ttgagatgag gtatatatct      300
c                                                                           301

```

<210> 305

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 305

```

gangtacagc gtggtcaagg taacaagaag aaaaaaatgt gagtggcatc ctgggatgag      60
cagggggaca gacctggaca gacacgttgt catttgctgc tgtgggtagg aaaatgggag      120
taaaggagga gaaacagata caaaatctcc aactcagtat taaggatttc tcatgcctag      180
aatattggta gaaacaagaa tacattcata tggcaaataa ctaaccatgg tggacaacaaa      240
ttctgggatt taagttggat accaangaaa ttgtattaaa agagctgttc atggaataag      300
a                                                                           301

```

<210> 306

<211> 8

<212> PRT

<213> Homo sapien

<400> 306

```

Val Leu Gly Trp Val Ala Glu Leu
1               5

```

<210> 307

<211> 637

<212> DNA

<213> Homo sapien

<400> 307

```

acagggratg aagggaaagg gagaggatga ggaagccccc ctggggattt ggtttgggtcc      60
ttgtgatcag gtggtctatg gggcttatcc ctacaaagaa gaatccagaa ataggggcac      120
attgaggaat gatacttgag cccaaagagc attcaatcat tgttttattt gccttmtttt      180
cacaccattg gtgagggagg gattaccacc ctggggttat gaagatgggtt gaacacccca      240
cacatagcac cggagatatg agatcaacag tttcttagcc atagagattc acagcccaga      300
gcaggaggac gcttgcacac catgcaggat gacatggggg atgcgctcgg gattggtgtg      360
aagaagcaag gactgttaga ggcaggcttt atagtaacaa gacggtgggg caaactctga      420
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actcattagg ctgagaacct tgtggaatgc acttgaccca sctgatagag gaagtagcca      540
ggtgggagcc ttcccagtg ggtgtgggac atatctggca agattttgtg gcactcctgg      600
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<210> 308

<211> 647

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(647)
 <223> n = A,T,C or G

<400> 308
 acgattttca ttatcatgta aatcgggtca ctcaaggggc caaccacagc tgggagccac 60
 tgctcagggg aaggttcata tgggactttc tactgcccac gggtctatac aggatataaa 120
 ggngcctcac agtatagatc tggtagcaaa gaagaagaaa caaacactga tctctttctg 180
 ccacccctct gacccttttg aactcctctg acccttttaga acaagcctac ctaatatctg 240
 ctagagaaaa gaccaacaac ggctcaaag gatctcttac catgaaggtc tcagctaatt 300
 cttggctaag atgtgggttc cacattaggt tctgaatatg gggggaagg tcaatttgct 360
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 gggaacaatg gctgagcata taaccatagg ttatggggaa caaaacaaca tcaaagtcac 480
 tgtatcaatt gccatgaaga cttgagggac ctgaatctac cgattcatct taaggcagca 540
 ggaccagttt gagtggcaac aatgcagcag cagaatcaat ggaaacaaca gaatgattgc 600
 aatgtccttt ttttctcct gcttctgact tgataaaagg ggaccgt 647

<210> 309
 <211> 460
 <212> DNA
 <213> Homo sapien

<400> 309
 acttttatagt ttaggctgga cattggaaaa aaaaaaagc cagaacaaca tgtgatagat 60
 aatatgattg gctgcacact tccagactga tgaatgatga acgtgatgga ctattgtatg 120
 gagcacatct tcagcaagag ggggaaatac tcatcatttt tggccagcag ttgtttgatc 180
 accaaacatc atgccagaat actcagcaaa ccttcttagc tcttgagaag tcaaagtccg 240
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 ctgggggtgt ggagcgaacc cgtcactagt ggacatgcag tggcagagct cctggtaacc 360
 acctagagga atacacaggc acatgtgtga tgccaagcgt gacacctgta gcactcaaat 420
 ttgtcttggt tttgtctttc ggtgtgtaag attcttaagt 460

<210> 310
 <211> 539
 <212> DNA
 <213> Homo sapien

<400> 310
 acgggactta tcaaataaag ataggaaaag aagaaaactc aaatattata ggcagaaatg 60
 ctaaaggttt taaaatatgt caggattgga agaaggcatg gataaagaac aaagttcagt 120
 taggaaagag aaacacagaa ggaagagaca caataaaagt cattatgtat tctgtgagaa 180
 gtcagacagt aagatttgtg ggaaatgggt tggtttgttg tatggtatgt attttagcaa 240
 taatctttat ggcagagaaa gctaaaatcc tttagcttgc gtgaatgatc acttgctgaa 300
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 ctagatagaa agccttagta tactcagcta ggaatagtga ttctgagggc acactgtgac 420
 atgattatgt cattacatgt atggtagtga tggggatgat aggaaggaag aacttatggc 480
 atattttcac cccacaaaa gtcagttaaa tattgggaca ctaaccatcc aggtcaaga 539

<210> 311
 <211> 526
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(526)

<223> n = A,T,C or G

<400> 311

caaatttgag ccaatgacat agaattttac aaatcaagaa gcttattctg gggccatttc	60
ttttgacgtt ttctctaaac tactaaagag gcattaatga tccataaatt atattatcta	120
catttacagc atttaaaatg tggtcagcat gaaatattag ctacagggga agctaaataa	180
attaaacatg gaataaagat ttgtccttaa atataatcta caagaagact ttgatatttg	240
tttttcacaa gtgaagcatt cttataaagt gtcataacct ttttggggaa actatgggaa	300
aaaatgggga aactctgaag ggttttaagt atcttacctg aagctacaga ctccataacc	360
tctctttaca gggagctcct gcagccccta cagaaatgag tggtgagat tcttgattgc	420
acagcaagag cttctcatct aaaccctttc cttttttagt atctgtgtat caagtataaa	480
agttctataa actgtagtnt acttatttta atccccaaag cacagt	526

<210> 312

<211> 500

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(500)

<223> n = A,T,C or G

<400> 312

cctctctctc cccaccccct gactctagag aactggggtt tctcccagta ctccagcaat	60
tcatttctga aagcagttga gccactttat tccaaagtac actgcagatg ttcaaaactct	120
ccatttctct ttccttcca cctgccagtt ttgctgactc tcaacttgct atgagtgtaa	180
gcatlaagga cattatgctt cttcgattct gaagacaggc cctgctcatg gatgactctg	240
gcttcttagg aaaatatatt tcttccaaaa tcagtaggaa atctaaactt atcccctctt	300
tgcatagtgc tagcagcttc agacatttgg ttaagaacct atgggaaaaa aaaaaatcct	360
tgctaagtgt gtttcctttg taaaccanga ttcttatttg nctggtatag aatatcagct	420
ctgaacgtgt ggtaaagatt ttgtgtttg aatataggag aaatcagttt gctgaaaagt	480
tagtcttaat tatctattgg	500

<210> 313

<211> 718

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(718)

<223> n = A,T,C or G

<400> 313

ggagatttgt gtggtttgca gccgaggag accaggaaga tctgcatggt gggaaggacc	60
tgatgataca gaggtgagaa ataagaaagg ctgctgactt taccatctga ggccacacat	120
ctgctgaaat ggagataatt aacatcacta gaaacagcaa gatgacaata taatgtctaa	180
gtagtgacat gtttttgcac atttccagcc ctttttaata tccacacaca caggaagcac	240
aaaaggaagc acagagatcc ctgggagaaa tgcccggccg ccatcttggg tcatcgatga	300
gcctcgccct gtgcctgntc ccgcttgtga gggaaggaca ttagaaaatg aattgatgtg	360
ttccttaag gatggcagga aaacagatcc tgtgtggat atttatttga acgggattac	420

agatttgaaa tgaagtcaca aagtgagcat taccaatgag aggaaaacag acgagaaaat	480
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aactggggag gagataccac ggggcagagg tcaggattct ggccctgctg cctaactgtg	600
cgttatacca atcatttcta tttctaccct caaacaagct gtngaataac tgacttacgg	660
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<210> 314

<211> 358

<212> DNA

<213> Homo sapien

<400> 314

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caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg tgtagtccaa	180
gctctcggta gtccagccac tgtgaaacat gtcctcttta gattaacctc gtggacgctc	240
ttgtttgtatt gctgaactgt agtgccctgt attttgcttc tgtctgtgaa ttctgttgct	300
tctggggcat ttccttgtga tgcagaggac caccacacag atgacagcaa tctgaatt	358

<210> 315

<211> 341

<212> DNA

<213> Homo sapien

<400> 315

taccacctcc ccgctggcac tgatgagccg catcaccatg gtcaccagca ccatgaaggc	60
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gacccccatt ctgaagatgt ctggaacctc taccagcagg atgatgatag ccccaatgac	180
agtcaccagc tccccgacca gccggatata gtccttaggg gtcattgtagg ctctctgaag	240
tagcttctgc tgtaagaggg tgttgtcccg ggggctcgtg cggttattgg tcctgggctt	300
gagggggcgg tagatgcagc acatgggtgaa gcagatgatg t	341

<210> 316

<211> 151

<212> DNA

<213> Homo sapien

<400> 316

agactgggca agactcttac gccccacact gcaatttggt cttgttgccg tatccattta	60
tgtgggcctt tctcgagttt ctgattataa acaccactgg agcgatgtgt tgactggact	120
cattcagggg gctctggttg caatattagt t	151

<210> 317

<211> 151

<212> DNA

<213> Homo sapien

<400> 317

agaactagtg gatcctaag aaataacctga aacatatatt ggcatttata aatggctcaa	60
atcttcatct atctctggcc ttaacctgg ctctgaggc tgcggccagc agatcccagg	120
ccagggctct gttcttgcca cacctgcttg a	151

<210> 318

<211> 151

<212> DNA

<213> Homo sapien

<400> 318

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actggtggga ggcgctgttt agttggctgt tttcagaggg gtctttcgga gggacctcct    60
gctgcaggct ggagtgtctt tattcctggc gggagaccgc acattccact gctgaggctg    120
tgggggcggg ttatcaggca gtgataaaca t                                     151
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<210> 319

<211> 151

<212> DNA

<213> Homo sapien

<400> 319

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aactagtggg tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta    60
catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg    120
taagattggg tttatgtgat tttagtgggt a                                     151
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<210> 320

<211> 150

<212> DNA

<213> Homo sapien

<400> 320

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aactagtggg tccactagtc cagtgtgggtg gaattccatt gtgttggggg tctagatcgc    60
gagcggctgc cctttttttt tttttttttg ggggggaatt tttttttttt aatagttatt    120
gagtgttcta cagcttacag taaataccat                                     150
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<210> 321

<211> 151

<212> DNA

<213> Homo sapien

<400> 321

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agcaactttg tttttcatcc aggttatttt aggccttagga tttcctctca cactgcagtt    60
tagggtggca ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg    120
tgctcttgag aaatcaaagt cttcatacac t                                     151
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<210> 322

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 322

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tttgggcttg gtcagtttgc cacagggtct ggagatgggt acagtcttct ggcattcggc    120
attgtgcagg gctcgcttca nacttccagt t                                     151
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<210> 323

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 323

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nagactcant tactaccag tttgtggtt twtgggagaa atgtaactgg acagtttagct	120
gttcaatyaa aaagacactt ancccatgtg g	151

<210> 324

<211> 461

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(461)

<223> n = A,T,C or G

<400> 324

acctgtgtgg aatttcagct ttcctcatgc aaaaggattt tgtatccccg gcctacttga	60
agaagtggc agctaaagga atccagggtt ttggttgac tgtaataacc tttgatgaaa	120
agagttacta cgaatcccat cttgggtcca gctatatcac tgacagcatg gtagaagact	180
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cacacaaatg caatagttgg tcaactgcatt tttacctgaa ccaaagctaa acccggtgtt	360
gccaccatgc accatggcat gccagagttc aacactgttg ctcttgaaaa ttgggtctga	420
aaaaacgcac aagagccccct gccctgccct agctgangca c	461

<210> 325

<211> 400

<212> DNA

<213> Homo sapien

<400> 325

acactgtttc catgttatgt ttctacacat tgctacctca gtgctcctgg aaacttagct	60
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agtaagagtg gtggcctatt tcagctgctt tgacaaaatg actggctcct gacttaacgt	180
tctataaatg aatgtgctga agcaaagtgc ccatgggtggc ggcaagaag agaaagatgt	240
gttttgtttt ggactctctg tggctccttc caatgctgtg ggtttccaac caggggaagg	300
gtcccttttg cattgccaaag tgccataacc atgagcacta cgctaccatg gttctgcctc	360
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<210> 326

<211> 1215

<212> DNA

<213> Homo sapien

<400> 326

ggaggactgc agcccgact cgcagccctg gcaggcgga ctggtcatgg aaaacgaatt	60
gttctgctcg ggcgtcctgg tgcattcgca gtgggtgctg tcagccgcac actgtttcca	120
gaactcctac accatcgggc tgggcctgca cagtcttgag gccgaccaag agccaggag	180

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ccagatggtg gaggccagcc tctccgtacg gcacccagag tacaacagac ccttgctcgc 240
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1215

```

<210> 327

<211> 220

<212> PRT

<213> Homo sapien

<400> 327

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Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
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Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
20          25          30
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
35          40          45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
50          55          60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
65          70          75          80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
85          90          95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
100         105         110
Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
115         120         125
Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
130         135         140
Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
145         150         155         160
Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
165         170         175
Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
180         185         190
Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
195         200         205
Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
210         215         220

```

<210> 328

<211> 234
 <212> DNA
 <213> Homo sapien

<400> 328
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<210> 329
 <211> 77
 <212> PRT
 <213> Homo sapien

<400> 329
 Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly Glu Asp Cys Ser
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 Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu
 20 25 30
 Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Thr
 35 40 45
 His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu
 50 55 60
 Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala
 65 70 75

<210> 330
 <211> 70
 <212> DNA
 <213> Homo sapien

<400> 330
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 gctgcagcca 70

<210> 331
 <211> 22
 <212> PRT
 <213> Homo sapien

<400> 331
 Gln His Asn Gly Pro Ile Pro Ser Leu Thr Pro Pro Ser Gly Ser Leu
 1 5 10 15
 Val Ser Gly Ser Cys Ser
 20

<210> 332
 <211> 2507
 <212> DNA
 <213> Homo sapien

<400> 332
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<211> 3030

<212> DNA

<213> Homo sapien

<400> 333

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<210> 334
 <211> 2417
 <212> DNA
 <213> Homo sapien

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<400> 334
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<211> 2984

<212> DNA

<213> Homo sapien

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<210> 336

<211> 147

<212> PRT

<213> Homo sapien

<400> 336

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Pro Lys Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln
35          40          45
Val Ile Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala
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Pro Glu Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln
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Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln
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<210> 337
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 <212> PRT
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 <212> PRT
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<211> 483
<212> DNA
<213> Homo sapien
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<211> 344
<212> DNA
<213> Homo sapien
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<212> DNA
<213> Homo sapien
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<210> 343

<211> 382

<212> DNA

<213> Homo sapien

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<210> 344

<211> 536

<212> DNA

<213> Homo sapien

<400> 344

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<211> 251

<212> DNA

<213> Homo sapien

<400> 345

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gcgtgggcca	ggaaatcaca	tcctacactg	cccaggagcc	agacacattt	atggaacaga	180
aaataacata	tcggatttgg	agagacactg	ccaactggct	ggagattaat	ccggacactg	240
gtgccatttc	c					251

<210> 346
 <211> 282
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(282)
 <223> n = A,T,C or G

<400> 346
 cgcgtctctg acactgtgat catgacaggg gttcaaacag aaagtgcctg ggccctcctt 60
 ctaagtcttg ttacccaaaa aaggaaaaag aaaagatctt ctcaagtaca aattctggga 120
 agggagacta tacctggctc ttgccctaag tgagaggtct tccctcccgc accaaaaaat 180
 agaaaggctt tctatttcac tggcccaggt agggggaagg agagtaactt tgagtctgtg 240
 ggtctcattt cccaaggtgc cttcaatgct catnaaaacc aa 282

<210> 347
 <211> 201
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(201)
 <223> n = A,T,C or G

<400> 347
 acacacataa tattataaaa tgccatctaa ttggaaggag ctttctatca ttgcaagtca 60
 taaatataac ttttaaaaa ntactancag cttttaccta ngctcctaaa tgcttgtaaa 120
 tctgagactg actggaccca cccagaccca gggcaaagat acatgttacc atatcatctt 180
 tataaagaat tttttttgt c 201

<210> 348
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 348
 ctgttaatca caacatttgt gcatacttg tgccaagtga gaaaatgttc taaaatcaca 60
 agagagaaca gtgccagaat gaaactgacc ctaagtccca ggtgcccctg ggcaggcaga 120
 aggagacact cccagcatgg aggaggggtt atcttttcat cctaggtcag gtctacaatg 180
 ggggaagggt ttattataga actcccaaca gccacactca ctctgccac ccaccgatg 240
 gccctgcctc c 251

<210> 349
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 349
 taaaaatcaa gccatttaat tgtatctttg aaggtaaaca atatatggga gctggatcac 60
 aacccttgag gatgccagag ctatgggtcc agaacatggt gtggtattat caacagagtt 120
 cagaagggtc tgaactctac gtgttaccag agaacataat gcaattcatg cattccactt 180
 agcaattttg taaaatacca gaaacagacc ccaagagtct ttcaagatga ggaaaattca 240

actcctggtt t

251

<210> 350

<211> 908

<212> DNA

<213> Homo sapien

<400> 350

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cggctggaat	tgctctggtt	atgatgacag	agaaaatgat	ctcttcctct	gtgacaccaa	180
cacctgtaaa	tttgatgggg	aatgtttaag	aattggagac	actgtgactt	gcgtctgtca	240
gttcaagtgc	aacaatgact	atgtgcctgt	gtgtggctcc	aatggggaga	gctaccagaa	300
tgagtgttac	ctgcgacagg	ctgcatgcaa	acagcagagt	gagatacttg	tggtgtcaga	360
aggatcatgt	gccacagtcc	atgaaggctc	tggagaaact	agtcaaaagg	agacatccac	420
ctgtgatatt	tgccagtttg	gtgcagaatg	tgacgaagat	gccgaggatg	tctgggtgtg	480
gtgtaatatt	gactgttctc	aaaccaactt	caatccccct	tgcgcttctg	atgggaaatc	540
ttatgataat	gcatgccaaa	tcaaagaagc	atcgtgtcag	aaacaggaga	aaattgaagt	600
catgtctttg	ggtcgatgtc	aagataacac	aactacaact	actaagtctg	aagatgggca	660
ttatgcaaga	acagattatg	cagagaatgc	taacaaatta	gaagaaagtg	ccagagaaca	720
ccacatacct	tgtccggaac	attacaatgg	cttctgcatg	catgggaagt	gtgagcattc	780
tatcaatatg	caggagccat	cttgccaggtg	tgatgctggt	tatactggac	aacactgtga	840
aaaaaaggac	tacagtgttc	tatacgttgc	tcccggctct	gtacgatttc	agtatgtctt	900
aatcgacg						908

<210> 351

<211> 472

<212> DNA

<213> Homo sapien

<400> 351

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gtcaaacctt	aatgccattg	ttattgtgaa	ttaggattaa	gtagtaattt	tcaaaattca	120
cattaacttg	attttaaaat	cagwtttgyg	agtcatttac	cacaagctaa	atgtgtacac	180
tatgataaaa	acaaccattg	tattcctgtt	tttctaaaca	gtcctaattt	ctaactactgt	240
atatatcctt	cgacatcaat	gaactttggt	ttcttttact	ccagtaataa	agtaggcaca	300
gatctgtcca	caacaaactt	gccctctcat	gccttgccct	tcaccatgct	ctgctccagg	360
tcagccccct	tttggcctgt	ttgttttgtc	aaaaaacctaa	tctgcttctt	gcttttcttg	420
gtaatatata	tttagggaag	atgttgcttt	gcccacacac	gaagcaaagt	aa	472

<210> 352

<211> 251

<212> DNA

<213> Homo sapien

<400> 352

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tgtggataag	gccagggtcaa	tggctgcaag	catgcagaga	aagaggtaga	tcggagcgtg	120
caggctgcgt	tccgtcctta	cgatgaagac	cacgatgcag	tttccaaaca	ttgccactac	180
atacatggaa	aggaggggga	agccaaccca	gaaatgggct	ttctctaata	ctgggatacc	240
aataagcaca	a					251

<210> 353

<211> 436

<212> DNA

<213> Homo sapien

<400> 353

tttttttttt	tttttttttt	tttttttaca	caatgcagtc	atltatttat	tgagtatgtg	60
cacattatgg	tattattact	atactgatta	tatttatcat	gtgacttcta	attaraaaat	120
gtatccaaaa	gcaaaacagc	agatatacaa	aattaaagag	acagaagata	gacattaaca	180
gataaggcaa	cttatacatt	gacaatccaa	atccaataca	tttaaacatt	tgggaaatga	240
gggggacaaa	tggaagccar	atcaaatttg	tgtaaaacta	ttcagtatgt	ttcccttgct	300
tcatgtctga	raaggctctc	ccttcaatgg	ggatgacaaa	ctccaaatgc	cacacaaatg	360
ttaacagaat	actagattca	cactggaacg	ggggtaaaga	agaaattatt	ttctataaaa	420
gggctcctaa	tgtagt					436

<210> 354

<211> 854

<212> DNA

<213> Homo sapien

<400> 354

ccttttctag	ttcaccagtt	ttctgcaagg	atgctgggta	gggagtgtct	gcaggaggag	60
caagtctgaa	accaaatacta	ggaaacatag	gaaacgagcc	aggcacaggg	ctgggtgggcc	120
atcaggggacc	accctttggg	ttgatatttt	gcttaatactg	catcttttga	gtaagatcat	180
ctggcagtag	aagctgttct	ccagggtacat	ttctctagct	catgtacaaa	aacatcctga	240
aggactttgt	cagggtgcctt	gctaaaagcc	agatgcgttc	ggcacttcct	tgggtctgagg	300
ttaattgcac	acctacaggg	actgggctca	tgctttcaag	tattttgtcc	tcacttttagg	360
gtgagtgaag	gatccccatt	ataggagcac	ttgggagaga	tcataataaa	gctgactctt	420
gagtacatgc	agtaattggg	tagatgtgtg	tgggtgtgtct	tcattcctgc	aagggtgctt	480
gttagggagt	gtttccagga	ggaacaagtc	tgaaaccaat	catgaaataa	atggtaggtg	540
tgaactggaa	aactaattca	aaagagagat	cgtgatatca	gtgtgggtga	tacaccttgg	600
caatatggaa	ggctctaat	tgcccatatt	tgaataata	attcagcttt	ttgtaataca	660
aaataacaaa	ggattgagaa	tcattggtgtc	taatgtataa	aagacccagg	aaacataaat	720
atatcaactg	cataaatgta	aaatgcatgt	gacccaagaa	ggcccccagg	tggcagacaa	780
cattgtaccc	attttccctt	ccaaaatgtg	agcggcgggc	ctgctgcttt	caaggctgtc	840
acacgggatg	tcag					854

<210> 355

<211> 676

<212> DNA

<213> Homo sapien

<400> 355

gaaattaagt	atgagctaaa	ttccctgtta	aaacctctag	gggtgacaga	tctcttcaac	60
cagggtcaaag	ctgatctttc	tggaatgtca	ccaaccaagg	gcctatatatt	atcaaaaagcc	120
atccacaagt	catacctgga	tgtcagcgaa	gagggcacgg	aggcagcagc	agccactggg	180
gacagcatcg	ctgtaaaaag	cctaccaatg	agagctcagt	tcaaggcgaa	ccaccccttc	240
ctgttcttta	taaggcacac	tcataccaac	acgatcctat	tctgtggcaa	gcttgccctc	300
ccctaatacag	atgggggtga	gtaaggctca	gagttgcaga	tgagggtgcag	agacaatcct	360
gtgactttcc	cacggccaaa	aagctgttca	cacctcacgc	acctctgtgc	ctcagtttgc	420
tcattctgcaa	aatagggtcta	ggattttctc	caaccatttc	atgagttgtg	aagctaaggc	480
tttgttaatc	atggaaaaag	gtagacttat	gcagaaaagc	tttctggctt	tcttatctgt	540
gggtgtctcat	ttgagtgctg	tccagtgaca	tgatcaagtc	aatgagtaaa	attttaaggg	600
attagatttt	cttgacttgt	atgtatctgt	gagatcttga	ataagtgacc	tgacatctct	660
gcttaaaagaa	aaccag					676

<210> 356

<211> 574

<212> DNA

<213> Homo sapien

<400> 356

tttttttttt tttttcagga aaacattctc ttactttatt tgcattctcag caaagggttct	60
catgtggcac ctgactggca tcaaaccaaa gtctcgtaggc caacaaagat gggccactca	120
caagcttccc attttagat ctgactgcct atgagtatct gacacctgtt cctctcttca	180
gtctcttagg gaggtctaaa tctgtctcag gtgtgctaag agtgccagcc caaggkggtc	240
aaaagtccac aaaactgcag tctttgctgg gatagtaagc caagcagtgc ctggacagca	300
gagttctttt cttgggcaac agataaccag acaggactct aatcgtgctc ttattcaaca	360
ttcttctgtc tctgcctaga ctggaataaa aagccaatct ctctcgtggc acagggaagg	420
agatacaagc tcgtttacat gtgatatagc taacaaaggc atctaccgaa gtctggtctg	480
gatagacggc acaggagagc cttaggctcag cgctgctggg tggaggacat tcctgagtc	540
agctttgcag cctttgtgca acagtacttt ccca	574

<210> 357

<211> 393

<212> DNA

<213> Homo sapien

<400> 357

tttttttttt tttttttttt tttttttttt tacagaatat aratgcttta tcaactgkact	60
taatatggkg kcttggtcac tatacttaaa aatgcaccac tcataaatat ttaattcagc	120
aagccacaac caaracttga ttttatcaac aaaaaccctt aaatataaac ggsaaaaaag	180
atagatataa ttattccagt ttttttaaaa cttaaaarat attccattgc cgaattaara	240
araarataag tgttatatgg aaagaagggc attcaagcac actaaaraaa cctgaggkaa	300
gcataatctg tacaaaatta aactgtcctt tttggcattt taacaaattt gcaacgkctt	360
tttttttctt tttctgtttt tttttttttt tac	393

<210> 358

<211> 630

<212> DNA

<213> Homo sapien

<400> 358

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gcatagagta gggaaagctaa tccagcacag ggaggtcaca gagacatccc taagggaagt	180
gagtttaaac tgagagaagc aagtgtctaa actgaaggat gtgttgaaga agaagggaga	240
gtagaacaat ttgggcagag ggaaccttat agaccctaag gtgggaagggt tcaaagaact	300
gaaagagagc tagaacagct ggagccgttc tccggtgtaa agaggagtca aagagataag	360
attaaagatg tgaagattaa gatcttggtg gcattcaggg attggcactt ctacaagaaa	420
tactgaagg gagtaatgtg acattacttt tcaacttcagg atggccattc taactccagg	480
gggtagactg gactaggtaa gactggaggg aggtagacct cttctaaggc ctgcgatagt	540
gaaagacaaa aataagtggg gaaattcagg ggatagtga aatcagtagg acttaatgag	600
caagccagag gttcctccac aacaaccagt	630

<210> 359

<211> 620

<212> DNA

<213> Homo sapien

<400> 359

acagcattcc aaaatataca tctagagact aarrgtaaat gctctatagt gaagaagtaa	60
taattaaaaa atgctactaa tatagaaaat ttataatcag aaaaataaat attcagggag	120

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ctcaccagaa gaataaagtg ctctgccagt tattaagga ttactgctgg tgaattaaat 180
atggcattcc ccaagggaaa tagagagatt cttctggatt atgttcaata tttatttcac 240
aggattaact gttttaggaa cagatataaa gcttcgccac ggaagagatg gacaaagcac 300
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tgcaacatta tgcttcattga ataatatgta gaaagaaggt ctgatgaaaa tgacatcctt 420
aatgtaagat aactttataa gaattctggg tcaaataaaa ttctttgaag aaaacatcca 480
aatgtcattg acttatcaaa tactatcttg gcatataacc tatgaaggca aaactaaaca 540
aacaaaaagc tcacaccaaa caaaaccatc aacttatttt gtattctata acatacgaga 600
ctgtaaagat gtgacagtgt 620

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<210> 360
<211> 431
<212> DNA
<213> Homo sapien

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<400> 360
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tactcatcat ttttggccag cagttgtttg atcaccaaac atcatgccag aatactcagc 180
aaaccttctt agctcttgag aagtcaaagt ccgggggaat ttattcctgg caattttaat 240
tggaactcctt atgtgagagc agcggctacc cagctggggg ggtggagcga acccgctact 300
agtggacatg cagtggcaga gctcctggta accacctaga ggaatacaca ggcacatgtg 360
tgatgccaag cgtgacacct gtagcactca aatttgtctt gtttttgtct ttcgggtgtg 420
agattcttag t 431

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<210> 361
<211> 351
<212> DNA
<213> Homo sapien

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<400> 361
acactgattt ccgatcaaaa gaatcatcat ctttaccttg acttttcagg gaattactga 60
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ttgggtcttc tggctctctg ccaagtttcc cagccactcg agggagaaat atcgggaggt 180
tgacttctt ccggggcttt cccgagggtt tcaccgtgag cctgcggcc ctacgggctg 240
caatcctgga ttcaatgtct gaaacctcgc tctctgcctg ctggacttct gaggccgtca 300
ctgccactct gtccctccagc tctgacagct cctcatctgt ggtcctgttg t 351

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<210> 362
<211> 463
<212> DNA
<213> Homo sapien

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<400> 362
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ccccggtcac agaaatgacc aggttgggtg ttttcagggt ccagtgtctg gtcagcagct 180
cgtaaaggat ttccgcgtcc gtgtcgcagg acagacgtat atacttccct ttcttcccca 240
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agttccattt ctacttttgg ttgatctggg tgccttccat gtgctggctc tgggcatagc 360
cacacttgca cacattctcc ctgataagca cgatggtgtg gacaggaagg aaggatttca 420
ttgagcctgc ttatggaaac tggatttgtt agcttaataa gac 463

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<210> 363
<211> 653

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<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(653)
<223> n = A,T,C or G

<400> 363
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 tgggaggcac tacgcaagat gggactgctg cctgggggtga gacatcctct ccttgagat 180
 ctaacgaac ttctcaccta tgagttgtaa agcagaaata cctgnactac agacgagtgc 240
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 attttgagaa tccntgggtcc agaattccat ttaccttctg ggccagatac caccagaatg 600
 cccgctccag attccctcag acctttgccg gtcccattat tggctcstggt ggt 653

<210> 364
<211> 401
<212> DNA
<213> Homo sapien

<400> 364
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 tgagaaagct caattataga tgcaaagtta taactaaact actatagtag taaagaaata 240
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 acgtgcatag taaatcttta tatttgctat ggcgttgca tagaggactt ggactgcaac 360
 aagtggatgc gcggaaaatg aaatcttctt caatagccca g 401

<210> 365
<211> 356
<212> DNA
<213> Homo sapien

<400> 365
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 taccagagca tcaagtctct gcagcaggtc attccttgggt aaagaaatga cttccacaaa 180
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 gactgtcacg atgtgtatag tacagtttga caagcctggg tccatacaga ccgctggaga 300
 acattcggca atgtccctt ttagccagat ttcttcttcg agctcccga gagcag 356

<210> 366
<211> 1851
<212> DNA
<213> Homo sapien

<400> 366
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cttccgtggt cttcattctt cttcaatagc cataaatctt ctagctctgg ctggctgttt 120
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gcacgagttt tactacttct gaattcccat tggcagaggc cagatgtaga gcagtcctct 780
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cttttcccca tttagtatta tgttggtgtt gggttgttca taggtgggtt ttattacttt 1800
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<210> 367

<211> 668

<212> DNA

<213> Homo sapien

<400> 367

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accrtataag agcagtgtt tggccattaa tttatcttcc attttagaca gctagtgya 180
gagtggatt tccatactca tctggaatat ttggatcagt gccatgttcc agcaacatta 240
acgcacattc atcttctctg cattgtacgg cctgtcagta ttagacccaa aaacaaatta 300
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<210> 368

<211> 1512

<212> DNA

<213> Homo sapien

<400> 368

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<210> 369

<211> 1853

<212> DNA

<213> Homo sapien

<400> 369

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<210> 370

<211> 2184

<212> DNA

<213> Homo sapien

<400> 370

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<210> 371
 <211> 1855
 <212> DNA
 <213> Homo sapien

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<400> 371
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<210> 372
 <211> 1059
 <212> DNA
 <213> Homo sapien

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<210> 373

<211> 1155

<212> DNA

<213> Homo sapien

<400> 373

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<210> 374

<211> 2000

<212> DNA

<213> Homo sapien

<400> 374

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<210> 375

<211> 2040

<212> DNA

<213> Homo sapien

<400> 375

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agcaacgtgg	gcacttctgg	agaccacgac	gactctgcta	tgaagacact	caggagcaag	180
atgggcaagt	ggtgccgcca	ctgcttcccc	tgctgcaggg	ggagtggcaa	gagcaacgtg	240
ggcgcttctg	gagaccacga	cgactctgct	atgaagacac	tcaggaacaa	gatgggcaag	300
tgggtgctgcc	actgcttccc	ctgctgcagg	gggagcggca	agagcaaggt	gggcgcttgg	360
ggagactacg	atgacagtgc	cttcatggag	cccaggtacc	acgtccgtgg	agaagatctg	420
gacaagctcc	acagagctgc	ctggtggggt	aaagtcacca	gaaaggatct	catcgtcatg	480
ctcagggaca	ctgacgtgaa	caagaaggac	aagcaaaaga	ggactgctct	acatctggcc	540
tctgccaatg	ggaattcaga	agtagtaaaa	ctcctgctgg	acagacgatg	tcaacttaat	600
gtccttgaca	acaaaaagag	gacagctctg	ataaaggccg	tacaatgcc	ggaagatgaa	660
tgtgcgtaa	tgttgctgga	acatggcact	gatccaaata	ttccagatga	gtatggaaat	720
accactctgc	actacgctat	ctataatgaa	gataaattaa	tggccaaagc	actgctctta	780
tatggtgctg	atatcgaatc	aaaaaacaag	catggcctca	caccactgtt	acttggtgta	840
catgagcaaa	aacagcaagt	cgtgaaatct	ttaatcaaga	aaaaagcgaa	tttaaatgca	900
ctggatagat	atggaaggac	tgctctcata	cttgctgtat	gttggtggatc	agcaagtata	960
gtcagccttc	tacttgagca	aaatattgat	gtatcttctc	aagatctatc	tggacagacg	1020
gccagagagt	atgctgtttc	tagtcatcat	catgtaattt	gccagttact	ttctgactac	1080
aaagaaaaac	agatgctaaa	aatctcttct	gaaaacagca	atccagaaca	agacttaaaag	1140
ctgacatcag	aggaagagtc	acaaagggttc	aaaggcagtg	aaaatagcca	gccagagaaa	1200
atgtctcaag	aaccagaaat	aaataaggat	ggtgatagag	aggttgaaga	agaaatgaag	1260
aagcatgaaa	gtaataatgt	gggattacta	gaaaacctga	ctaattggtgt	cactgctggc	1320
aatgggtgata	atggattaat	tcctcaaagg	aagagcagaa	cacctgaaaa	tcagcaattt	1380

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cctgacaacg aaagtgaaga gtatcacaga atttgcgaat tagtttctga ctacaaagaa 1440
aaacagatgc caaaatactc ttctgaaaac agcaaccag aacaagactt aaagctgaca 1500
tcagaggaag agtcacaaag gcttgagggc agtgaaaatg gccagccaga gaaaagatct 1560
caagaaccag aaataaataa ggatgggat agagagctag aaaattttat ggctatcgaa 1620
gaaatgaaga agcacggaag tactcatgtc ggattcccag aaaacctgac taatgggtgcc 1680
actgctggca atgggtgatga tggattaatt cctccaagga agagcagaac acctgaaagc 1740
cagcaatttc ctgacactga gaatgaagag tatcacagt acgaacaaaa tgatactcag 1800
aagcaatttt gtgaagaaca gaacactgga atattacacg atgagattct gattcatgaa 1860
gaaaagcaga tagaagtggg tgaaaaaatg aattctgagc tttctcttag ttgtaagaaa 1920
gaaaagaca tcttgcataa aaatagtacg ttgcgggaag aaattgccat gctaagactg 1980
gagctagaca caatgaaaca tcagagccag ctaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040

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<210> 376

<211> 329

<212> PRT

<213> Homo sapien

<400> 376

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20     25     30
Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
35     40     45
Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
50     55     60
Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
65     70     75     80
Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
85     90     95
Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
100    105    110
His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
115    120    125
Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
130    135    140
Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
145    150    155    160
Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
165    170    175
Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
180    185    190
Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
195    200    205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
210    215    220
Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
225    230    235    240
Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
245    250    255
Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
260    265    270
Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
275    280    285
Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu

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290 295 300
 Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu
 305 310 315 320
 Ser Met Leu Phe Leu Val Ile Ile Met
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<210> 377
 <211> 148
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
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 <223> Xaa = Any Amino Acid

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 20 25 30
 Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys
 35 40 45
 Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
 50 55 60
 Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
 65 70 75 80
 Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
 85 90 95
 Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
 100 105 110
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
 115 120 125
 Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser
 130 135 140
 Lys Asn Lys Val
 145

<210> 378
 <211> 1719
 <212> PRT
 <213> Homo sapien

<400> 378
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 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn

Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp
 530 535 540
 Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln
 545 550 555 560
 Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val
 565 570 575
 Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn
 580 585 590
 Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu
 595 600 605
 Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp
 610 615 620
 Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys
 625 630 635 640
 Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys
 645 650 655
 Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
 660 665 670
 Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
 675 680 685
 Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
 690 695 700
 Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
 705 710 715 720
 Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser
 725 730 735
 His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln
 740 745 750
 Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys
 755 760 765
 Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser
 770 775 780
 Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp
 785 790 795 800
 Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly
 805 810 815
 Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn
 820 825 830
 Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe
 835 840 845
 Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser
 850 855 860
 Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn
 865 870 875 880
 Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu
 885 890 895
 Glu Gly Ser Glu Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile
 900 905 910
 Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn
 915 920 925
 Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro
 930 935 940
 Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu
 945 950 955 960
 Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe

965 970 975
 Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His
 980 985 990
 Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser
 995 1000 1005
 Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu
 1010 1015 1020
 Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His
 1025 1030 1035 104
 Gln Ser Gln Leu Pro Arg Thr His Met Val Val Glu Val Asp Ser Met
 1045 1050 1055
 Pro Ala Ala Ser Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met
 1060 1065 1070
 Gly Lys Trp Cys Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys
 1075 1080 1085
 Ser Asn Val Gly Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr
 1090 1095 1100
 Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys
 1105 1110 1115 112
 Arg Gly Ser Gly Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp
 1125 1130 1135
 Ser Ala Met Lys Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His
 1140 1145 1150
 Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp
 1155 1160 1165
 Gly Asp Tyr Asp Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg
 1170 1175 1180
 Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val
 1185 1190 1195 120
 Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys
 1205 1210 1215
 Lys Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly
 1220 1225 1230
 Asn Ser Glu Val Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn
 1235 1240 1245
 Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys
 1250 1255 1260
 Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro
 1265 1270 1275 128
 Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr
 1285 1290 1295
 Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp
 1300 1305 1310
 Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val
 1315 1320 1325
 His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala
 1330 1335 1340
 Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala
 1345 1350 1355 136
 Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn
 1365 1370 1375
 Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr
 1380 1385 1390
 Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr
 1395 1400 1405

Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu
 1410 1415 1420
 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly
 1425 1430 1435 144
 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn
 1445 1450 1455
 Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser
 1460 1465 1470
 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly
 1475 1480 1485
 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu
 1490 1495 1500
 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys
 1505 1510 1515 152
 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser
 1525 1530 1535
 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu
 1540 1545 1550
 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser
 1555 1560 1565
 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe
 1570 1575 1580
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe
 1585 1590 1595 160
 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly
 1605 1610 1615
 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro
 1620 1625 1630
 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln
 1635 1640 1645
 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile
 1650 1655 1660
 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser
 1665 1670 1675 168
 Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn
 1685 1690 1695
 Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr
 1700 1705 1710
 Met Lys His Gln Ser Gln Leu
 1715

<210> 379

<211> 656

<212> PRT

<213> Homo sapien

<400> 379

Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
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 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60

Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
 385 390 395 400
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
 405 410 415
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
 420 425 430
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
 435 440 445
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
 450 455 460
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
 465 470 475 480
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
 485 490 495
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu

500 505 510
 Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys
 515 520 525
 Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly
 530 535 540
 Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser
 545 550 555 560
 Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr
 565 570 575
 His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln
 580 585 590
 Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln
 595 600 605
 Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys
 610 615 620
 Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile
 625 630 635 640
 Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
 645 650 655

<210> 380

<211> 671

<212> PRT

<213> Homo sapien

<400> 380

Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
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 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn

225					230					235				240
Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys	Leu	Met	Ala
				245					250					255
Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys	Asn	Lys	His
			260					265					270	
Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys	Gln	Gln	Val
		275					280					285		
Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala	Leu	Asp	Arg
	290					295					300			Tyr
Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	Ser	Ala	Ser
305					310					315				320
Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser	Ser	Gln	Asp
			325						330					335
Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser	His	His	His
			340				345						350	Val
Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys
	355					360						365		Ile
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln	Asp	Leu	Lys	Leu	Thr	Ser
	370				375						380			Glu
Glu	Glu	Ser	Gln	Arg	Phe	Lys	Gly	Ser	Glu	Asn	Ser	Gln	Pro	Glu
385				390						395				Lys
Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys	Asp	Gly	Asp	Arg	Glu	Val
			405						410				415	Glu
Glu	Glu	Met	Lys	Lys	His	Glu	Ser	Asn	Asn	Val	Gly	Leu	Leu	Glu
		420						425				430		Asn
Leu	Thr	Asn	Gly	Val	Thr	Ala	Gly	Asn	Gly	Asp	Asn	Gly	Leu	Ile
	435					440						445		Pro
Gln	Arg	Lys	Ser	Arg	Thr	Pro	Glu	Asn	Gln	Gln	Phe	Pro	Asp	Asn
	450				455					460				Glu
Ser	Glu	Glu	Tyr	His	Arg	Ile	Cys	Glu	Leu	Val	Ser	Asp	Tyr	Lys
465				470						475				Glu
Lys	Gln	Met	Pro	Lys	Tyr	Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Gln
			485					490					495	Asp
Leu	Lys	Leu	Thr	Ser	Glu	Glu	Glu	Ser	Gln	Arg	Leu	Glu	Gly	Ser
		500					505					510		Glu
Asn	Gly	Gln	Pro	Glu	Lys	Arg	Ser	Gln	Glu	Pro	Glu	Ile	Asn	Lys
	515					520					525			Asp
Gly	Asp	Arg	Glu	Leu	Glu	Asn	Phe	Met	Ala	Ile	Glu	Glu	Met	Lys
	530				535				540					Lys
His	Gly	Ser	Thr	His	Val	Gly	Phe	Pro	Glu	Asn	Leu	Thr	Asn	Gly
545				550					555					Ala
Thr	Ala	Gly	Asn	Gly	Asp	Asp	Gly	Leu	Ile	Pro	Pro	Arg	Lys	Ser
			565					570					575	Arg
Thr	Pro	Glu	Ser	Gln	Gln	Phe	Pro	Asp	Thr	Glu	Asn	Glu	Glu	Tyr
		580					585					590		His
Ser	Asp	Glu	Gln	Asn	Asp	Thr	Gln	Lys	Gln	Phe	Cys	Glu	Glu	Gln
	595					600					605			Asn
Thr	Gly	Ile	Leu	His	Asp	Glu	Ile	Leu	Ile	His	Glu	Glu	Lys	Gln
	610				615				620					Ile
Glu	Val	Val	Glu	Lys	Met	Asn	Ser	Glu	Leu	Ser	Leu	Ser	Cys	Lys
625				630					635					Lys
Glu	Lys	Asp	Ile	Leu	His	Glu	Asn	Ser	Thr	Leu	Arg	Glu	Glu	Ile
			645					650					655	Ala
Met	Leu	Arg	Leu	Glu	Leu	Asp	Thr	Met	Lys	His	Gln	Ser	Gln	Leu
		660					665					670		

<210> 381
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 381
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 ggtaacatgc ttcccctaag ggtatcccaa cccaggggcc tcaccatgac ctctgagggg 120
 ccaatatccc aggagaagca ttggggagtt gggggcaggt gaaggacca ggactcacac 180
 atcctggggc tccaaggcag aggagagggt cctcaagaag gtcaggagga aaatccgtaa 240
 caagcagtca g 251

<210> 382
 <211> 3279
 <212> DNA
 <213> Homo sapiens

<400> 382
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 atgctggagg gtgtcaggaa gtgatcgggc tctggggcag ggaggagggg tggggagtgt 120
 cactgggagg ggacatcctg cagaaggtag gagtgaagca acacccgctg caggggaggg 180
 gagagccctg cggcacctgg gggagcagag ggagcagcac ctgcccaggc ctgggaggag 240
 gggcctggag ggcgtgagga ggagcagggg ggctgcatgg ctggagttag ggatcagggg 300
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<210> 383

<211> 155

<212> PRT

<213> Homo sapiens

<400> 383

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His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
      35                                40                                45

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
      50                                55                                60

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
      65                                70                                75                                80

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
      85                                90                                95

Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
      100                               105                               110

Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
      115                               120                               125

Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
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Ala Leu Glu Arg Gly His Leu Val Arg Glu
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<210> 384
<211> 557
<212> DNA
<213> Homo sapiens

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ccttcttatt tatgtgaaca actgtttgtc tttttttgta tcttttttaa actgtaaagt 480
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aaaaaaaaa aaaaaaa 557

<210> 385
<211> 337
<212> DNA
<213> Homo sapiens

<400> 385
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tctcaaagcc atctgctgtc ttcgagtagc gacacatcat cactcctgca ttgttgatca 180
aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240
tatcagacag gtccagtttc cgcaccaaca cctgctgggt ccctgtcgtg gtctggatct 300
ctttggccac caattcccc tttccacat cccggca 337

<210> 386
<211> 300
<212> DNA
<213> Homo sapiens

<400> 386
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gcgaccttgg ccgaaggct ctagcaagga cccaccgacc ccagccgcgg cggcggcggc 180
gcggactttg cccggtgtgt ggggcggagc ggactgcgtg tccgcggacg ggcagcgaag 240
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<210> 387
<211> 537
<212> DNA
<213> Homo sapiens

<400> 387
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tgaaccagga ccggcttctg ggcggctgaa aggggcaagg aggcaaggac ccgtctctc 180
ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttcctc agcactgagg 240
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<210> 388

<211> 520

<212> DNA

<213> Homo sapiens

<400> 388

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tcataactcaa ttgatggTTa ttagacaatt ccatttcttt ctggTTatta taaacagaaa 420
atctttctc ttctcattac cagtaaaggc tcttggtatc tttctgTTgg aatgatttct 480
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<210> 389

<211> 365

<212> DNA

<213> Homo sapiens

<400> 389

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cccaggaaac cttcagacta cttcctctg cttcagcaa ggggcgttg ccacattctc 300
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<210> 390

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(221)

<223> n = A,T,C or G

<400> 390

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gctctangag tctgancnga ntcgTTgcc cantntgaca naaggaaagg cggagcttat 180
tcaaagTcta gagggagtgg aggagTTaag gctggatttc a 221
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<210> 391

<211> 325

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(325)
<223> n = A,T,C or G

<400> 391
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naanttngat ntccanagcc ctaccatcn tagttctgct ctcccacgg ntaccagccc 240
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gagacctccg gctactacta tgacc 325

<210> 392
<211> 277
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(277)
<223> n = A,T,C or G

<400> 392
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antaccanga accgncatgn cttanaaacn ncctggtttn tgggttnntc aatgactgca 180
tgcagtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggcgg 240
ctgaggatac agcgcgcggt cctgtgttgc tggggaa 277

<210> 393
<211> 566
<212> DNA
<213> Homo sapiens

<400> 393
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gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga ttaaattcag cctaaacggt 120
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cattctctgc ctgagtttta atttttgtcc aaagttattt taatctatac aattaaaagc 540
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<210> 394
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)...(384)

<223> n = A,T,C or G

<400> 394

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agggtagcaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360
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<210> 395

<211> 399

<212> DNA

<213> Homo sapiens

<400> 395

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caagttctct ttggaaagcc tgggcattct ctactacag acctctgacc atgggacggg 360
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<210> 396

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(403)

<223> n = A,T,C or G

<400> 396

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gttttagggga gggagtggag gataaaaagaa ggaaaaaaaag aagagtgaga aaacctattt 360
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<210> 397

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(100)

<223> n = A,T,C or G

<400> 397

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 tccatccccg ctcttggttg gtnacagaat gactgacaaa 100

<210> 398

<211> 278

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 398

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 ccacctggac atctggaagt cagcggcctg gatgaaagag cggacttcac ctggggcgat 120
 tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgagggtg actcatcatg 180
 ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
 ctatggccgc ttcattangt ggctcaacaa ggagaagg 278

<210> 399

<211> 298

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(298)

<223> n = A,T,C or G

<400> 399

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 ggggtgccng catggagcgc atgggcgcgg gcctgggcca cggcatggat cgcgtgggct 120
 ccgagatcga gcgcattggc ctggatcatg accgcatggg ctccgtggag cgcattgggct 180
 ccggcattga gcgcattggc ccgctgggccc tcgaccacat ggccctccanc attgancgca 240
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<210> 400

<211> 548

<212> DNA

<213> Homo sapiens

<400> 400

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 caaagaacca cacgctaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180
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<210> 401
<211> 355
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(355)
<223> n = A,T,C or G

<400> 401
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cccttttgca ttgccaagtg ccataaccat gagcactact ctaccatggn tctgc 355

<210> 402
<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(407)
<223> n = A,T,C or G

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gaataaagat aaaaaagaga aggacattac aaaggtgggc ctgacctttg ataaatctca 240
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<210> 403
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 403
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tagagaacaa gacctactca gtcataaaca aaaaggcaga caccaacatg gatctcatgg 180
gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt tggcacaaca 240
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gga 303

<210> 404
<211> 225
<212> DNA
<213> Homo sapiens

<400> 404
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acattttcca ctcggtgttc catagttgtt aagtgtatca gatgtgttgg gcatgtgaat 180
ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225

<210> 405
<211> 334
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (334)
<223> n = A,T,C or G

<400> 405
gagctgttat actgtgagtt ctactaggaa atcatcaaat ctgagggttg tctggaggac 60
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cactctccac tctctcanng tggatccac ccct 334

<210> 406
<211> 216
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (216)
<223> n = A,T,C or G

<400> 406
tttcatacct aatgaggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60
gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120
acnaaacaca aatttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180
actgccaaag aatnttcaag aaggaggact gccant 216

<210> 407
<211> 413
<212> DNA
<213> Homo sapiens

<400> 407
gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60
gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120
gtacaacatt gcacccagtg tcagattcta cacctggcca ctgaggaagc aagagttaat 180
cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240

```
ggaaaattgt catttgtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt ttccctgtca 360
tgggagttcc agaaaaagtt aaaacagaca atgggccagg ttctgtagta aag 413
```

<210> 408

<211> 183

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(183)

<223> n = A,T,C or G

<400> 408

```
ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60
tncttaacta gttaatcctt aaagggctan ntaatcctta actagtcctt ccattgtgag 120
cattatcctt ccagtattcn ccttctnttt tattttactcc ttccctggcta cccatgtact 180
ntt 183
```

<210> 409

<211> 250

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(250)

<223> n = A,T,C or G

<400> 409

```
cccacgcatg ataagctctt tatttctgta agtcctgcta ggaaatcatc aaatctgacg 60
gtgggtttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180
gcttcccagt gccccagga cagcgtgggc tatgtttaca gcgcntcctt gctggggggg 240
ggcntatgc 250
```

<210> 410

<211> 306

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(306)

<223> n = A,T,C or G

<400> 410

```
ggctggtttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60
agtcttgcaa tcccatttgc aggatccgtc tgtgcacatg cctctgtaga gagcagcatt 120
cccagggacc ttggaaacag ttggcactgt aagggtgctt ctccccaaaga cacatcctaa 180
aagggtgtgt aatggtgaaa accgcttcct tctttattgc cccttcttat ttatgtgaac 240
nactggtttg ctttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300
tcntgc 306
```

<210> 411
<211> 261
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(261)
<223> n = A,T,C or G

<400> 411
agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tattaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaattgc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa ggngaggcaa a 261

<210> 412
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 412
gttcaatgtt acctgacatt tctacaacac cccactcacc gatgtattcg ttgcccagtg 60
ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgcccagg aaatactacg 120
actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180
ctggggagatt tcaactgggtta cattgaattc ccaaactacc cangcaatta cccagccaac 240
a 241

<210> 413
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(231)
<223> n = A,T,C or G

<400> 413
aactcttaca atccaagtga ctcattctgtg tgcttgaatc ctttccactg tctcatctcc 60
ctcatccaag tttctagtac cttctctttg ttgtgaagga taatcaaact gaacaacaaa 120
aagtttactc tcctcatttg gaacctaaaa actctcttct tcctgggtct gagggctcca 180
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231

<210> 414
<211> 234
<212> DNA
<213> Homo sapiens

<400> 414

```
actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
gtgagccaag gagggagggt cttcctttgg catgggatgg ggatgaagta aggagagggg 180
ctggaccccc tggaagctga ttcactatgg ggggaggtgt attgaagtcc tcca      234
```

<210> 415

<211> 217

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(217)

<223> n = A,T,C or G

<400> 415

```
gcataggatt aagactgagt atcttttcta cattctttta actttctaag gggcacttct 60
caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cactttctca 120
cacctagcaa tagtagaatt cagtcctact tctgaggcca gaagaatggg tcagaaaaat 180
antggattat aaaaaataac aattaagaaa aataatc      217
```

<210> 416

<211> 213

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(213)

<223> n = A,T,C or G

<400> 416

```
atgcatatnt aaagganact gcctcgcttt tagaagacat ctggnctgct ctctgcatga 60
ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120
cgaatgcaag gtgggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180
atattggaac agatggagtc tctactacaa aag      213
```

<210> 417

<211> 303

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(303)

<223> n = A,T,C or G

<400> 417

```
nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60
gtgggaaagg ctttactctg agttcaaate ttcaagccca tcagagagtc cacactggag 120
agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180
ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt ggggaagggt 240
tcantcaaag ttcgtatctt caaatccatc ngaaggngcca cagtatanan aaacctttta 300
agt      303
```


<210> 418
 <211> 328
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(328)
 <223> n = A,T,C or G

```
<400> 418
tttttggcgg tgggtggggca gggacggggac angagtctca ctctgttgcc caggctggag 60
tgcacaggca tgatctcggc tcaactacaac ccctgcctcc catgtccaag cgattcttgt 120
gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacaccca gctagttttt 180
gtatttttag tagagacagg gtttcacccat gttggccagg ctggtctcaa actcctnacc 240
tcagnggtca ggctgggtctc aaactcctga cctcaagtga tctgcccacc tcagcctccc 300
aaagtgctan gattacaggc cgtgagcc 328
```

<210> 419
 <211> 389
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(389)
 <223> n = A,T,C or G

```
<400> 419
cctcctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatag 60
acccctgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120
cttgtttctt ctctgtggct ccattcatag cacagttgtt gcaactgaggc ttgtgcaggc 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggg gtgccaggca 240
ccggttctcc agccaccaac ctcaactcgt cccgcaaagt gcacatcagt tcttctaccc 300
taaaggtagg accaaagggc atctgctttt ctgaagtcct ctgctctatc agccatcacg 360
tggcagccac tcnggctgtg tcgacgcgg 389
```

<210> 420
 <211> 408
 <212> DNA
 <213> Homo sapiens

```
<400> 420
gttcctccta actcctgcca gaaacagctc tctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggtt tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgctatg acaaacctgg caagcccg 408
```

<210> 421
 <211> 352
 <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(352)

<223> n = A,T,C or G

<400> 421

```
gctcaaaaat ctttttactg atnggcatgg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacaggtct tttttgggtc cttcttctcc accacnatac attgcagtc 180
ctccttcttg aagattcttt ggcagttgtc tttgtcataa cccacaggtg tagaaacaag 240
ggtgcaacat gaaatttctg tttcgtagca agtgcattgc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttcct gg 352
```

<210> 422

<211> 337

<212> DNA

<213> Homo sapiens

<400> 422

```
atgccaccat gctggcaatg cagcgggcgg tcgaaggcct gcataatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
gcatagcaa ggtgccggcg atcgcgcgcg cgtcaatcct ggccaaggtc agccgtgatc 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcggcggg cataagggtc 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
gcttcttccg ccggtacggc tggcctatga aaattat 337
```

<210> 423

<211> 310

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(310)

<223> n = A,T,C or G

<400> 423

```
gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60
aggagaatga ggcctggcct gggagccctg tgcctactan aagcncatta gattatccat 120
tactgacag aacaggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtc 180
tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240
gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgccc 300
tccgagttta 310
```

<210> 424

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(370)

<223> n = A,T,C or G

<400> 424

```
gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60
ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120
cactgacaga acaggtcttt tttgggtcct tcttctccac cacgatatac ttgcagtcct 180
ccttcttgaa gattcttttg cagttgtctt tgtcataacc cacaggtgta gaaacatcct 240
ggttgaatct cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300
cacgaagggtg gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360
tccgtcgacg                                     370
```

<210> 425

<211> 216

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(216)

<223> n = A,T,C or G

<400> 425

```
aattgctatn ntttatTTTg ccactcaaaa taattaccaa aaaaaaaaaa tnttaaatga 60
taacaacnca acatcaaggn aaananaaca ggaatggntg acctngcata aatnggccga 120
anattatcca ttatnttaag ggttgacttc aggntacagc acacagacaa acatgcccag 180
gaggntntca ggaccgctcg atgtnttntg aggagg                                     216
```

<210> 426

<211> 596

<212> DNA

<213> Homo sapiens

<400> 426

```
cttccagtga ggataaccct gttgccccgg gccgagggttc tccattaggc tctgattgat 60
tggcagtcag tgatggaagg gtgttctgat cattccgact gcccgaaggg tcgctggcca 120
gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatggtga 180
gctgtccttg tattttgatt aacctaattg cttcccagc acgactcgga ttcagctgga 240
gacatcacgg caacttttaa tgaaatgatt tgaagggccca ttaagaggca cttcccgtta 300
ttaggcagtt catctgcact gataacttct tggcagctga gctgggtcgga gctgtggccc 360
aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
ggtggatggc cttttcagct ttaacccaat ttgcactgcc ttggaagtgt agccaggaga 480
atacactcat atactcgtgg gcttagaggg cacagcagat gtcattgggt tactgcctga 540
gtcccgtcgg tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct     596
```

<210> 427

<211> 107

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(107)

<223> n = A,T,C or G

<400> 427

```
gaagaattca agttaggttt attcaaaggg cttacngaga atcctanacc caggncccag 60
```

cccggggagca gccttanaga gctcctgttt gactgcccgg ctcagn 107

<210> 428

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(38)

<223> n = A,T,C or G

<400> 428

gaacttcena anaangactt tattcactat ttacatt 38

<210> 429

<211> 544

<212> DNA

<213> Homo sapiens

<400> 429

ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60
attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120
atatccacga actcttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180
tttggtatggg ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tcactcgtt 240
gccttcact tcagttacac ctactcacc atctctcct gttggttctg tgctgcttca 300
agatactaag cccacatttg agatgcagca gccatctccc ccaattcctc ctgtccatcc 360
tgatgtgcag ttaaaaaatc tggcctttta tgatgtcctt gatgttctca tcaagcccac 420
gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480
acctcaacaa gtttagagaga tatgcatatc cagggatttt ttgccagggtg gtaggagaga 540
ttat 544

<210> 430

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(507)

<223> n = A,T,C or G

<400> 430

cttatcncaa tggggctccc aaacttggtt gtgcagtgga aactccgggg gaattttgaa 60
gaacactgac acccatcttc caccgccaga ctctgattta attgggctgc agtgagaaca 120
gagcatcaat ttaaaaagct gcccagaatg ttntcctggg cagcgttgtg atctttgccn 180
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgagggg gttccaggag 240
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300
caagaaggag gactgcaagt atatcggttg ggagaagaag gacccaaaaa agacctgttc 360
tgtcagtga tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420
cattctcctc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480
ttttgagcaa aaaaaaaaaa aaaaaaa 507

<210> 431

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(392)

<223> n = A,T,C or G

<400> 431

```

gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtcttgggtt ttccaacaga 240
catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300
acaaaagtga tgttgtagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360
gcaatgagtc tggcttttac tctgctgttt ct 392

```

<210> 432

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(387)

<223> n = A,T,C or G

<400> 432

```

ggtatcanta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
aaatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
ngtagtccaa gctctcggna gtccagccac tngaaacat gctcccttta gattaacctc 180
gtggacnctn ttgttgnatt gtctgaactg tagngccctg tattttgctt ctgtctgnga 240
attctgttgc ttctggggca ttctcttngn atgcagagga ccaccacaca gatgacagca 300
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgtac aggaccggga 360
acaacgtata gaacactgga gtccttt 387

```

<210> 433

<211> 281

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(281)

<223> n = A,T,C or G

<400> 433

```

ttcaactagc anagaanact gcttcagggg gtgtaaaatg aaaggcttcc acgcagttat 60
ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180
atcgccgtgg ctattcctcn ttgntattac accagngagg ntctctgtnt gccactgggt 240
tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281

```

<210> 434

<211> 484

<212> DNA

<213> Homo sapiens

<400> 434

```

ttttaaaata agcatttagt gctcagtcct tactgagtag tctttctctc cctcctctg 60
aatttaattc tttcaacttg caatttgcaa ggattacaca tttcactgtg atgtatattg 120
tggtgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtgaa tccatcttgc 180
tttttccccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acaggtgaat tggatgggtc tcagaacctt ttcacccaga 300
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaaccc 360
tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag taccatgtc 480
ttaa
484

```

<210> 435

<211> 424

<212> DNA

<213> Homo sapiens

<400> 435

```

gcgcccgtca ggcagggtca ctttctgcct tccacgtcct ccttcaagga agcccatgt 60
gggtagcttt caatatcgca gggtcttact cctctgcctc tataagctca aaccaccaa 120
cgatcgggca agtaaacccc ctccctcgcc gacttcggaa ctggcgagag ttcagcgcag 180
atgggcctgt ggggaggggg caagatagat gagggggagc ggcatgggtc ggggtgaccc 240
cttgagagaga ggaaaaggc cacaagaggg gctgccaccg ccactaacgg agatggcct 300
ggtagagacc tttgggggtc tggaaacctc ggactcccca tgctctaact cccacactct 360
gctatcagaa acttaaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac
424

```

<210> 436

<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(667)

<223> n = A,T,C or G

<400> 436

```

accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcctggccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataagggtgc 120
agcctcttct ggaattcctc tgatttcaaa gtctcactct caagttcttg aaaacgaggg 180
cagttcctga aaggcaggta tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacagggct 300
gccaggtttg tcatagcact catcaaagtc cgggtcaacgt ctgtgcttcg aatataaacc 360
tgttcatgtt tataggactc attcaagaat tttctatata tctttcttat atactctcca 420
agttcataat gctgctccat gccagctgg gtgagttggc caaatccttg tggccatgag 480
gattccttta tggggctcagt gggaaaagtg tcaatgggac ttcggtctcc atgccgaaac 540
accaaagtca caaacttcaa ctcttggtc agtacacttc ggtctagcca gaaaaaaagc 600
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660
tgttgag
667

```

<210> 437

<211> 693

<212> DNA

<213> Homo sapiens

<400> 437

```
ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaaag ctggattggc aactaggac tctaccatac cgggttttgt 120
taaagctcag gttaggaggc tgataagctt ggaaggaaact tcagacagct ttttcagatc 180
ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtaactct ctatttttcac cctcttctgt tctactctct ggcaatcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatgtt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcacta ttgggggggac agccagcacc ttttagctttc 420
atlttgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
acacctaact gctgttgctc ctgaggtggg gaaagacaga tatagagctt acagtattta 540
tcctattttc aggcactgag ggctgtgggg taccttgtgg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcatcatg tgctctcttg gctgaaaatg acc                                     693
```

<210> 438

<211> 360

<212> DNA

<213> Homo sapiens

<400> 438

```
ctgcttatca caatgaatgt tctctggggc agcgttgtga tctttgccac ctctgtgact 60
ttatgcaatg catcatgcta tttcatacct aatgagggag ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaaag acaactgcc aagaatcttc aagaaggagg 180
actgcaagta tatctggtgg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360
```

<210> 439

<211> 431

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(431)

<223> n = A,T,C or G

<400> 439

```
gttcctnnta actcctgcc aaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tgccaggggc agcaagcctt agccttggct tcttgtttct gcttttttct tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggg gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag t                                     431
```

<210> 440

<211> 523

<212> DNA

<213> Homo sapiens

```

<400> 440
agagataaaag cttaggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatccttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaattgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360
taaaaattaa aacctctttg tgtcccttgg tcttggaaca tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaat acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcattctga tgagaacaag cta 523

```

```

<210> 441
<211> 430
<212> DNA
<213> Homo sapiens

```

```

<400> 441
gttctctcta actcctgcca gaaacagctc tcttcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggtc tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgaccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag 430

```

```

<210> 442
<211> 362
<212> DNA
<213> Homo sapiens

```

```

<400> 442
ctaaggaatt agtagtggtc ccattcacttg tttggagtgt gctattctaa aagattttga 60
tttcttgga tgaacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120
cttctcttct gatacttgta aattaatctt ttattgcact tgttttgacc attaaactat 180
atgttttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc 362

```

```

<210> 443
<211> 624
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(624)
<223> n = A,T,C or G

```

```

<400> 443
tttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60
ttgaaagaat taaattcaga ggaggggaga gaaagagtac tcagtaggga ctgagcacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240

```



```
cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaacttgg ctccctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaatgaac 360
taacgcctac aaaacactta aacatagata acataggtgc aagtactatg tatctggtac 420
atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaata 480
agtacagaga gagggcactt aaaccaacta agggcctgga ggggaagggtt cctggaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatTTAAact 600
ttgtccctat ctgctaaaca gatc 624
```

<210> 444

<211> 425

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(425)

<223> n = A,T,C or G

<400> 444

```
gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtgggtg gtcagcaaata ccttgaatgc 180
tgcttaatgt gagaggttgg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcatectgt gaagagccaa 360
ggaggcacca gggcataagt gagtagactt atggtcgacg cggccgcgaa tttagtagta 420
gtaga 425
```

<210> 445

<211> 414

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(414)

<223> n = A,T,C or G

<400> 445

```
catgtttatg nttttggatt actttgggca cctagtgttt ctaaatcgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcattgtggc agattattgg atgtagtctt ctttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtggtggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaatgact aggcttctcc tcttgtattt tgaagcagtg 360
tgggtgctgg attgataaaa aaaaaaaaaa tgcacgcggc cgcgaattta gtag 414
```

<210> 446

<211> 631

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(631)

<223> n = A,T,C or G

<400> 446

```

acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcagggtgtg 120
atgctgggtta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttggtc 180
ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240
ctgtcatctg tgtggtggtc ctctgcatca caagggccaa actttaggta atagcattgg 300
actgagatth gttaactttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360
gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatggt tcacagtggc tggactaccg agagcttgga ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tgttgccctg catttggtgtg 540
aatctacacc aatgaaaaca tgtactacag ctatatattga ttatgtatgg atatatttga 600
aatagtatac attgtcttga tgttttttct g                                     631

```

<210> 447

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(585)

<223> n = A,T,C or G

<400> 447

```

ccttgggaaa antntcacaa tataaagggt cgtagacttt actccaaatt ccaaaaaggt 60
cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taaggggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagttcttga aaacgagggc 180
agttcctgaa aggcaggtat agcaactgat cttcagaaaag aggaactgtg tgcaccggga 240
tgggctgcca gagtaggata ggattccaga tgctgacacc ttctggggga aacagggctg 300
ccaggtttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
gttcatgttt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480
attcctttat ggggtcagtg ggaaagggtg caatgggact tcggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttggcta gtacacttcg gtcta                                     585

```

<210> 448

<211> 93

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(93)

<223> n = A,T,C or G

<400> 448

```

tgctcgtggg tcattctgan nncggaactg accntgccag ccctgccgan gggccnccat 60
ggctccctag tgccctggag agganggggc tag                                     93

```

<210> 449

<211> 706

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(706)
 <223> n = A,T,C or G

<400> 449
 ccaagttcat gctntgtgct ggacgctgga caggggggcaa aagcnnttgc tegtgggtca 60
 ttctgancac cgaactgacc atgccagccc tgccgatggt cctccatggc tccctagtgc 120
 cctggagagg aggtgtctag tcagagagta gtcctggaag gtggcctctg ngaggagcca 180
 cggggacagc atcctgcaga tggtcgggcg cgtcccattc gccattcagg ctgcgcaact 240
 gttgggaagg gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 300
 gtgctgcaag gcgattaagt tgggtaacgc caggggtttc ccagtcncga cgttgtaaaa 360
 cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcattgcacg 420
 cgtacgtaag cttggatcct cttagcgggc cgcctactac tactaaattc gcggccgcgt 480
 cgacgtggga tccncactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540
 cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600
 aacagggttg acctgggagg tggagggttg aatgagctga gatcaggccn ctgcncacca 660
 gcatggatga cagagtga aa ctccatctta aaaaaaaaaa aaaaaa 706

<210> 450
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 450
 gagacggagt gtcactctgt tgcccaggct ggagtgcagc aagacactgt ctaagaaaaa 60
 acagttttta aaggtaaaac aacataaaaa gaaatatcct atagtggaaa taagagagtc 120
 aatgaggct gagaacttta caaagggatc ttacagacat gtcgccaata tcaactgcatg 180
 agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ggtacaattc 240
 caagtcaggt agtgaaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300
 agagacactg tcagagagtt aaaaagttag ttctatccat gaggtgattc cacagtcttc 360
 tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420
 tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggg cgacgcggcc 480
 gcgaatttag tag 493

<210> 451
 <211> 501
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(501)
 <223> n = A,T,C or G

<400> 451
 gggcgcgtcc cattcgccat tcaggctgcy caactgttgg gaagggcgat cggctgcgggc 60
 ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 120
 aacgccaggg ttttcccagt cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180
 tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240
 gcggccgcct actactacta aattcgcggc cgcgtcgacg tgggatccnc actgagagag 300
 tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacia 360
 cgcncacagac actcacagct actcaggagg ctgagaacag gttgaacctg ggagggtggag 420
 gttgcaatga gctgagatca ggcnctgcn ccccagcatg gatgacagag tgaaactcca 480

tctttaaaaaa aaaaaaaaaa a 501

<210> 452
 <211> 51
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(51)
 <223> n = A,T,C or G

<400> 452
 agacgggtttc accntttacaa cnccttttag gatgggnntt ggggagcaag c 51

<210> 453
 <211> 317
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(317)
 <223> n = A,T,C or G

<400> 453
 tacatcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60
 acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatgggtc tcagaacctat 120
 ttcacccana cagcctggtt ctatcctgtt taataaatta gtttgggttc tctacatgca 180
 taacaaaccc tgctccaatc tgtcacataa aagtctgtga cttgaagttt antcagcacc 240
 cccaccaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300
 taccatgctc tttatta 317

<210> 454
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 454
 ttcgaggtac aatcaactct cagagtgtag tttccttcta tagatgagtc agcatthaata 60
 taagccacgc cagctctttg aaggagtctt gaattctcct ctgctcactc agtagaacca 120
 agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180
 ccttcctttt tcagtgttcc aaagctcctc acaatttcat gaacaacagc t 231

<210> 455
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 455
 taccaaagag ggcataataa tcagtctcac agtaggggtc accatcctcc aagtgaaaaa 60
 cattgttccg aatgggcttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120
 gtttcaacgc attgatgact tctccaagga tcttcctttg gcatcgacca cattcagggg 180
 caaagaattt ctcatagcac agctcacaat acagggtccc tttctcctct a 231

<210> 456
<211> 231
<212> DNA
<213> Homo sapiens

<400> 456
ttggcaggta cccttacaaa gaagacacca taccttatgc gttattaggt ggaataatca 60
ttccattcag tattatcggt attattcttg gagaaacct gtctgtttac tgtaaccttt 120
tgcactcaaa ttcctttatc aggaataact acatagccac tatttacaaa gccattggaa 180
cctttttatt tgggtgcagct gctagtcagt ccctgactga cattgccaag t 231

<210> 457
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(231)
<223> n = A,T,C or G

<400> 457
cgagggtaccc aggggtctga aaatctctnn ttantagtc gatagcaaaa ttgttcatca 60
gcattcctta atatgatctt gctataatta gatttttctc cattagagtt catcacagttt 120
tatttgattt tattagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc 180
agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgt g 231

<210> 458
<211> 231
<212> DNA
<213> Homo sapiens

<400> 458
aggtctgggt cccccactt ccactcccct ctactctctc taggactggg ctgggccaag 60
agaagagggg tggtaggga agccgttgag acctgaagcc ccacctcta ccttccttca 120
acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180
ggctcctgggt taggcatttt ggggggcccag accccaggag aagaagattc t 231

<210> 459
<211> 231
<212> DNA
<213> Homo sapiens

<400> 459
ggtaccgagg ctgctgaca cagagaaacc ccaacgcgag gaaaggaatg gccagccaca 60
ccttcgcgaa acctgtggtg gccaccagt cctaacggga caggacagag agacagagca 120
gccctgcact gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc 180
actatacaca gtcacgtcc caatgagaaa caagaaggag caccctccac a 231

<210> 460
<211> 231
<212> DNA
<213> Homo sapiens

<400> 460

```
gcagggtataa catgctgcaa caacagatgt gactaggaac ggccggtgac atggggaggg 60
cctatcaccc tattcttggg ggctgcttct tcacagtgat catgaagcct agcagcaaat 120
cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca 180
gtggagcttg gtccagcctc cagtccaccc ctaccaggct taaggataga a 231
```

<210> 461

<211> 231

<212> DNA

<213> Homo sapiens

<400> 461

```
cgagggtttga gaagctctaa tgtgcagggg agccgagaag caggcggcct agggaggggtc 60
gcgtgtgctc cagaagagtg tgtgcatgcc agaggggaaa caggcgcctg tgtgtcctgg 120
gtgggggttca gtgaggagtg ggaaattggt tcagcagaac caagccgttg ggtgaataag 180
agggggattc catggcactg atagagccct atagtctcag agctgggaat t 231
```

<210> 462

<211> 231

<212> DNA

<213> Homo sapiens

<400> 462

```
aggtaccctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60
gggtcatgca agtataaaaa ttaaaaaaaaa aagacttcat gccaatctc atatgatgtg 120
gaagaactgt tagagagacc aacagggtag tgggttagag atttccagag tcttacattt 180
tctagaggag gtattttaatt tcttctcact catccagtgt tgtatttagg a 231
```

<210> 463

<211> 231

<212> DNA

<213> Homo sapiens

<400> 463

```
tactccagcc tggtgacaga gcgagaccct atcacgcgcc cccacccccc caaaaaaaaa 60
actgagtaga cagggtgcct cttggcatgg taagtcttaa gtcccctccc agatctgtga 120
catttgacag gtgtcttttc ctctggacct cgggtgtcccc atctgagtga gaaaaggcag 180
tggggaggtg gatcttccag tcgaagcggc atagaagccc gtgtgaaaag c 231
```

<210> 464

<211> 231

<212> DNA

<213> Homo sapiens

<400> 464

```
gtactctaag attttatcta agttgccttt tctgggtggg aaagttaaac cttagtgact 60
aaggacatca catatgaaga atgtttaagt tggaggtggc aacgtgaatt gcaaacaggg 120
cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180
gggtgccagcg caccagctag atgctctgta acttctaggc cccattttcc c 231
```

<210> 465

<211> 231

<212> DNA

<213> Homo sapiens

<400> 465

```

catgttgttg tagctgtggg aatgctggct gcatctcaga caggggtaac ttcagctcct 60
gtggcaaat agcaacaaat tctgacatca tatttatggg ttctgtatct ttgttgatga 120
aggatggcac aatttttgc tgtgttcata atatactcag attagttcag ctccatcaga 180
taaactggag acatgcagga cattagggta gtgttgtagc tctggtaatg a 231

```

<210> 466

<211> 231

<212> DNA

<213> Homo sapiens

<400> 466

```

caggtaacctc tttccattgg atactgtgct agcaagcatg ctctccgggg tttttttaat 60
ggccttcgaa cagaacttgc cacataccca ggtataatag tttctaacat ttgccagga 120
cctgtgcaat caaatattgt ggagaattcc ctagctggag aagtcacaaa gactataggc 180
aataatggag accagtccca caagatgaca accagtcgtt gtgtgcggct g 231

```

<210> 467

<211> 311

<212> DNA

<213> Homo sapiens

<400> 467

```

gtacacctcg gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg 60
tggcggcttt tctccttttt catcaagact cctcagcagg gagccagac cagcctgcac 120
tgtgccttaa cagaaggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg 180
gcatgggtct ctgccaagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt 240
tgtgacctgc tgggcctccc aatagactaa caggcagtgc cagtgggacc caagagaaga 300
ctgcagcaga c 311

```

<210> 468

<211> 3112

<212> DNA

<213> Homo sapiens

<400> 468

```

cattgtgttg ggagaaaaac agaggggaga tttgtgtggc tgcagccgag ggagaccagg 60
aagatctgca tgggtgggaag gacctgatga tacagagttt gataggagac aattaaaggc 120
tggaaggcac tggatgcctg atgatgaagt ggactttcaa actggggcac tactgaaacg 180
atgggatggc cagagacaca ggagatgagt tggagcaagc tcaataacaa agtggttcaa 240
cgaggacttg gaattgcatg gagctggagc tgaagtttag cccaattgtt tactagttga 300
gtgaatgtgg atgattggat gatcatttct catctctgag cctcaggttc cccatccata 360
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<210> 469

<211> 2229

<212> DNA

<213> Homo sapiens

<400> 469

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<210> 470

<211> 2426

<212> DNA

<213> Homo sapiens

<400> 470

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<210> 471

<211> 812

<212> DNA

<213> Homo sapiens

<400> 471

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<211> 515

<212> DNA

<213> Homo sapiens

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<223> n = A,T,C or G

<400> 472

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